

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ST. GEORGE-HYSLOP, PETER H  
ROMMENS, JOHANNA M  
FRASER, PAUL E

(ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE

(iii) NUMBER OF SEQUENCES: 183

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK  
(B) STREET: 600 South Avenue West  
(C) CITY: Westfield  
(D) STATE: New Jersey  
(E) COUNTRY: U.S.A.  
(F) ZIP: 07090

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Microsoft Word, Version 6.0c

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/509,359  
(B) FILING DATE: 31-JUL-95  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Palisi, Thomas M.  
(B) REGISTRATION NUMBER: 36629

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 654-5000  
(B) TELEFAX: (908) 654-7866

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2791 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGNAAGC GTATACCTAA	120
TCTGGGAGCC TGCAAGTGAC AACAGCCTTT GCGGTCCTTA GACAGCTTGG CCTGGAGGAG	180
AACACATGAA AGAAAGAACC TCAAGAGGCT TTGTTTTCTG TGAAACAGTA TTTCTATACA	240
GTTGCTCCAA TGACAGAGTT ACCTGCACCG TTGTCCTACT TCCAGAATGC ACAGATGTCT	300

GAGGACAACC	ACCTGAGCAA	TACTGTACGT	AGCCAGAATG	ACAATAGAGA	ACGGCAGGAG	360
CACAACGACA	GACGGAGCCT	TGGCCACCCT	GAGCCATTAT	CTAATGGACG	ACCCCAGGGT	420
AACTCCCGGC	AGGTGGTGGA	GCAAGATGAG	GAAGAAGATG	AGGAGCTGAC	ATTGAAATAT	480
GGCGCCAAGC	ATGTGATCAT	GCTCTTTGTC	CCTGTGACTC	TCTGCATGGT	GGTGGTCGTG	540
GCTACCATTA	AGTCAGTCAG	CTTTTATACC	CGGAAGGATG	GGCAGCTAAT	CTATACCCCA	600
TTACAGAAAG	ATACCGAGAC	TGTGGGCCAG	AGAGCCCTGC	ACTCAATTCT	GAATGCTGCC	660
ATCATGATCA	GTGTCATTGT	TGTCATGACT	ATCCTCCTGG	TGGTTCTGTA	TAAATACAGG	720
TGCTATAAAG	TCATCCATGC	CTGGCTTATT	ATATCATCTC	TATTGTTGCT	GTTCTTTTTT	780
TCATTCAATTT	ACTTGGGGGA	AGTGTTTAAA	ACCTATAACG	TTGCTGTGGA	CTACATTACT	840
GTTGCACTCC	TGATCTGGAA	TTTGGGTGTG	GTGGGAATGA	TTTCCATTCA	CTGGAAAGGT	900
CCACTTCGAC	TCCAGCAGGC	ATATCTCATT	ATGATTAGTG	CCCTCATGGC	CCTGGTGTTT	960
ATCAAGTACC	TCCCTGAATG	GACTGCGTGG	CTCATCTTGG	CTGTGATTTT	AGTATATGAT	1020
TTAGTGGCTG	TTTTGTGTCC	GAAAGGTCCA	CTTCGTATGC	TGGTTGAAAC	AGCTCAGGAG	1080
AGAAATGAAA	CGCTTTTTTC	AGCTCTCATT	TACTCCTCAA	CAATGGTGTG	GTTGGTGAAT	1140
ATGGCAGAAG	GAGACCCGGA	AGCTCAAAGG	AGAGTATCCA	AAAATTCCAA	GTATAATGCA	1200
GAAAGCACAG	AAAGGGAGTC	ACAAGACACT	GTTGCAGAGA	ATGATGATGG	CGGGTTCAGT	1260
GAGGAATGGG	AAGCCCAGAG	GGACAGTCAT	CTAGGGCCTC	ATCGCTCTAC	ACCTGAGTCA	1320
CGAGCTGCTG	TCCAGGAACT	TTCCAGCAGT	ATCCTCGCTG	GTGAAGACCC	AGAGGAAAGG	1380
GGAGTAAAAC	TTGGATTGGG	AGATTTTCATT	TTCTACAGTG	TTCTGGTTGG	TAAAGCCTCA	1440
GCAACAGCCA	GTGGAGACTG	GAACACAACC	ATAGCCTGTT	TCGTAGCCAT	ATTAATTGGT	1500
TTGTGCCTTA	CATTATTACT	CCTTGCCATT	TTCAAGAAAG	CATTGCCAGC	TCTTCCAATC	1560
TCCATCACCT	TTGGGCTTGT	TTTCTACTTT	GCCACAGATT	ATCTTGTACA	GCCTTTTATG	1620
GACCAATTAG	CATTCCATCA	ATTTTATATC	TAGCATATTT	GCGGTTAGAA	TCCCATGGAT	1680
GTTTCTTCTT	TGACTATAAC	CAAATCTGGG	GAGGACAAAG	GTGATTTTCC	TGTGTCCACA	1740
TCTAACAAAG	TCAAGATTCC	CGGCTGGACT	TTTGCAGCTT	CCTTCCAAGT	CTTCTGACC	1800
ACCTTGCACT	ATTGGACTTT	GGAAGGAGGT	GCCTATAGAA	AACGATTTTG	AACATACTTC	1860
ATCGCAGTGG	ACTGTGTCCT	CGGTGCAGAA	ACTACCAGAT	TTGAGGGACG	AGGTCAAGGA	1920
GATATGATAG	GCCCGBAAGT	TGCTGTGCCC	CATCAGCAGC	TTGACGCGTG	GTCACAGGAC	1980
GATTTCACTG	ACACTGCGAA	CTCTCAGGAC	TACCGGTTAC	CAAGAGGTTA	GGTGAAGTGG	2040
TTTAAACCAA	ACGGAACCTC	TCATCTTAAA	CTACACGTTG	AAAATCAACC	CAATAATTCT	2100
GTATTAAGTG	AATTCTGAAC	TTTTCAGGAG	GTACTGTGAG	GAAGAGCAGG	CACCAGCAGC	2160
AGAATGGGGA	ATGGAGAGGT	GGGCAGGGGT	TCCAGCTTCC	CTTTGATTTT	TTGCTGCAGA	2220

CTCATCCTTT TTAAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA	2280
TGCCTTTGGC AATTCTTCTT CTCAAGCACT GACACTCATT ACCGTCTGTG ATTGCCATTT	2340
CTTCCCAAGG CCAGTCTGAA CCTGAGGTTG CTTTATCCTA AAAGTTTTAA CCTCAGGTTT	2400
CAAATTCAGT AAATTTTGGG AACAGTACAG CTATTTCTCA TCAATTCTCT ATCATGTTGA	2460
AGTCAAATTT GGATTTTCCA CCAAATTCTG AATTTGTAGA CATACTTGTA CGCTCACTTG	2520
CCCCAGATGC CTCCTCTGTC CTCATTCTTC TCTCCACAC AAGCAGTCTT TTTCTACAGC	2580
CAGTAAGGCA GCTCTGTCGT GGTAGCAGAT GGTCCCACTT ATTCTAGGGT CTTACTCTTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 467 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met	1	5	10	15
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn	20	25	30	
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu	35	40	45	
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu	50	55	60	
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	65	70	75	80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val	85	90	95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln	100	105	110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125	
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140	
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155	160

Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe	
				165					170					175		
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala	
			180					185					190			
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Leu	Gly	Val	Val	
		195					200					205				
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala	
	210					215					220					
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr	
225					230					235					240	
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr	
				245					250					255		
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val	
			260					265					270			
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr	
		275					280					285				
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu	
	290					295					300					
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	Tyr	Asn	Ala	Glu	Ser	Thr	
305					310					315					320	
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe	
				325					330					335		
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg	
			340					345					350			
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile	
		355					360					365				
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	
	370					375					380					
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala	
385					390					395					400	
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	
				405					410					415		
Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu	
			420					425					430			
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala	
		435					440					445				
Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	His	Gln	
	450					455					460					
Phe	Tyr	Ile														
465																

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCANACANC	GGCAGCTGAG	GCGGAAACCT	AGGCTGCGAG	CCGGCCGCCC	GGGCGCGGAG	60
AGAGAAGGAA	CCAACACAAG	ACAGCAGCCC	TTCGAGGTCT	TTAGGCAGCT	TGGAGGAGAA	120
CACATGAGAG	AAAGAATCCC	AAGAGGTTTT	GTTTTCTTTG	AGAAGGTATT	TCTGTCCAGC	180
TGCTCCAATG	ACAGAGATAC	CTGCACCTTT	GTCTACTTTC	CAGAATGCCC	AGATGTCTGA	240
GGACAGCCAC	TCCAGCAGCG	CCATCCGGAG	CCAGAATGAC	AGCCAAGAAC	GGCAGCAGCA	300
GCATGACAGG	CAGAGACTTG	ACAACCCTGA	GCCAATATCT	AATGGGCGGC	CCCAGAGTAA	360
CTCAAGACAG	GTGGTGGAAC	AAGATGAGGA	GGAAGACGAA	GAGCTGACAT	TGAAATATGG	420
AGCCAAGCAT	GTCATCATGC	TCTTTGTCCC	CGTGACCCTC	TGCATGGTCG	TCGTCTGGGC	480
CACCATCAAA	TCAGTCAGCT	TCTATACCCG	GAAGGACGGT	CAGCTAATCT	ACACCCCATT	540
CACAGAAGAC	ACTGAGACTG	TAGGCCAAAG	AGCCCTGCAC	TCGATCCTGA	ATGCGGCCAT	600
CATGATCAGT	GTCATTGTCA	TTATGACCAT	CCTCCTGGTG	GTCTGTATA	AATACAGGTG	660
CTACAAGGTC	ATCCACGCCT	GGCTTATTAT	TTCATCTCTG	TTGTTGCTGT	TCTTTTTTTC	720
GTTCATTTAC	TTAGGGGAAG	TATTTAAGAC	CTACAATGTC	KCCGTGGACT	ACGTTACAGT	780
AGCACTCCTA	ATCTGGAATT	GGGGTGTGGT	CGGGATGATT	GCCATCCACT	GGAAAGGCCC	840
CCTTCGACTG	CAGCAGGCGT	ATCTCATTAT	GATCAGTGCC	CTCATGGCCC	TGGTATTTAT	900
CAAGTACCTC	CCCGAATGGA	CCGCATGGCT	CATCTTGGCT	GTGATTTTCA	TATATGATTT	960
GGTGGCTGTT	TTATGTCCCA	AAGGCCCACT	TCGTATGCTG	GTTGAAACAG	CTCAGGAAAG	1020
AAATGAGACT	CTCTTTCCAG	CTCTTATCTA	TTCTCAACA	ATGGTGTGGT	TGGTGAATAT	1080
GGCTGAAGGA	GACCCAGAAG	CCCAAAGGAG	GGTACCCAAG	AACCCCAAGT	ATAACACACA	1140
AAGAGCGGAG	AGAGAGACAC	AGGACAGTGG	TTCTGGGAAC	GATGATGGTG	GCTTCAGTGA	1200
GGAGTGGGAG	GCCCAAAGAG	ACAGTCACCT	GGGGCCTCAT	CGCTCCACTC	CCGAGTCAAG	1260
AGCTGCTGTC	CAGGAACCTT	CTGGGAGCAT	TCTAACGAGT	GAAGACCCGG	AGGAAAGAGG	1320
AGTAAACTTT	GGACTGGGAG	ATTTTCATTTT	CTACAGTGTT	CTGGTTGGTA	AGGCCTCAGC	1380
AACCGCCAGT	GGAGACTGGA	ACACAACCAT	AGCCTGCTTK	GTAGCCATAC	TGATCGGCCT	1440
GTGCCTTANA	TTACTCCTGC	TCGCCATTTA	CAAGAAAGGG	TNGCCAGCCC	NCCCCATCTC	1500

CATCACCTTC GGGTTCGTGT TCTNCTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA 1560  
 CCAACTTGCA TTCCATCAGT TTTATATCTA GCCTTTCTGC AGTTAGAACA TGGATGTTTC 1620  
 TTCTTTGATT ATCAAAAACA CAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT 1680  
 TCCTGTGTCC TCAGCTAACA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCCGA 1740  
 GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAAGGAAG CGTCTACAGA GGAACGGTTT 1800  
 CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA 1860  
 AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GGMCCGTGGG CATGGAGATT 1920  
 TACCCGCAC 1929

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Glu	Ile	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Ser	His	Ser	Ser	Ser	Ala	Ile	Arg	Ser	Gln	Asn	Asp	Ser
			20					25					30		
Gln	Glu	Arg	Gln	Gln	Gln	His	Asp	Arg	Gln	Arg	Leu	Asp	Asn	Pro	Glu
		35					40					45			
Pro	Ile	Ser	Asn	Gly	Arg	Pro	Gln	Ser	Asn	Ser	Arg	Gln	Val	Val	Glu
	50					55					60				
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys
65					70					75					80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
			85						90					95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
			100					105					110		
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg
		115					120					125			
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val
	130					135					140				
Ile	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys
145					150					155					160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe
			165						170					175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Xaa

180					185					190					
Val	Asp	Tyr	Val	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Trp	Gly	Val	Val
		195					200					205			
Gly	Met	Ile	Ala	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala
	210					215					220				
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr
225					230					235					240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr
				245					250					255	
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val
			260					265					270		
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr
		275					280					285			
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu
	290					295					300				
Ala	Gln	Arg	Arg	Val	Pro	Lys	Asn	Pro	Lys	Tyr	Asn	Thr	Gln	Arg	Ala
305					310					315					320
Glu	Arg	Glu	Thr	Gln	Asp	Ser	Gly	Ser	Gly	Asn	Asp	Asp	Gly	Gly	Phe
				325					330					335	
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg
			340					345					350		
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Gly	Ser	Ile
		355					360					365			
Leu	Thr	Ser	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly
	370					375					380				
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala
385					390					395					400
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Xaa	Val	Ala	Ile	Leu	Ile
				405					410					415	
Gly	Leu	Cys	Leu	Xaa	Leu	Leu	Leu	Leu	Ala	Ile	Tyr	Lys	Lys	Gly	Xaa
			420					425					430		
Pro	Ala	Xaa	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Phe	Val	Phe	Xaa	Phe	Ala
		435					440					445			
Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	His	Gln
	450					455					460				
Phe	Tyr	Ile													
465															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3087 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA	CGAGGGAAAT	GCTGTTTGCT	CGAAGACGTC	TCAGGGCGCA	GGTGCCTTGG	60
GCCGGGATTA	GTAGCCGTCT	GAAGTGGAGT	GGAGTAGGAG	AAAGAGGAAG	CGTCTTGGGC	120
TGGGTCTGCT	TGAGCAACTG	GTGAAACTCC	GCGCCTCAGC	CCCCGGGTGT	GTCCTTGTCC	180
AGGGGCGACG	AGCATTCTGG	GCGAAGTCCG	CACSCCTCTT	GTTTCGAGGCG	GAAGACGGGG	240
TCTGATSCTT	TCTCCTTGGT	CGGGMCTGTC	TCGAGGCATG	CATGTCCAGT	GAATCTTGTG	300
TTTGCTGCTG	CTTCCCTCTC	AGATTCTTCT	CACCGTTGTG	GTCAGCTCTG	CTTTAGGCAN	360
TATTAATCCA	TAGTGGAGGC	TGGGATGGGT	GAGAGAATTG	AGGTGACTTT	TCCATAATTC	420
AGACCTAATC	TGGGAGCCTG	CAAGTGACAA	CAGCCTTTCG	GGTCCTTAGA	CAGCTTGGCC	480
TGGAGGAGAA	CACATGAAAG	AAAGAACCTC	AAGAGGCTTT	GTTTTCTGTG	AAACAGTATT	540
TCTATACAGT	TGCTCCAATG	ACAGAGTTAC	CTGCACCGTT	GTCCTACTTC	CAGAATGCAC	600
AGATGTCTGA	GGACAACCAC	CTGAGCAATA	CTAATGACAA	TAGAGAACGG	CAGGAGCACA	660
ACGACAGACG	GAGCCTTGGC	CACCCTGAGC	CATTATCTAA	TGGACGACCC	CAGGGTAACT	720
CCCGGCAGGT	GGTGGAGCAA	GATGAGGAAG	AAGATGAGGA	GCTGACATTG	AAATATGGCG	780
CCAAGCATGT	GATCATGCTC	TTTGTCCCTG	TGACTCTCTG	CATGGTGGTG	GTCGTGGCTA	840
CCATTAAGTC	AGTCAGCTTT	TATACCCGGA	AGGATGGGCA	GCTAATCTAT	ACCCCATTC	900
CAGAAGATAC	CGAGACTGTG	GGCCAGAGAG	CCCTGCACTC	AATTCTGAAT	GCTGCCATCA	960
TGATCAGTGT	CATTGTTGTC	ATGACTATCC	TCCTGGTGGT	TCTGTATAAA	TACAGGTGCT	1020
ATAAGGTCAT	CCATGCCTGG	CTTATTATAT	CATCTCTATT	GTTGCTGTTC	TTTTTTTCAT	1080
TCATTTACTT	GGGGGAAGTG	TTTAAACCT	ATAACGTTGC	TGTGGACTAC	ATTACTGTTG	1140
CACTCCTGAT	CTGGAATTTG	GGTGTGGTGG	GAATGATTTT	CATTCACTGG	AAAGGTCCAC	1200
TTGACTCCA	GCAGGCATAT	CTCATTATGA	TTAGTGCCCT	CATGGCCCTG	GTGTTTATCA	1260
AGTACCTCCC	TGAATGGACT	GCGTGGCTCA	TCTTGGCTGT	GATTTTCAGTA	TATGATTTAG	1320
TGGCTGTTTT	GTGTCCGAAA	GGTCCACTTC	GTATGCTGGT	TGAAACAGCT	CAGGAGAGAA	1380
ATGAAACGCT	TTTTCCAGCT	CTCATTTACT	CCTCAACAAT	GGTGTGGTTG	GTGAATATGG	1440
CAGAAGGAGA	CCCGGAAGCT	CAAAGGAGAG	TATCCAAAAA	TTCCAAGTAT	AATGCAGAAA	1500
GCACAGAAA	GGAGTCACAA	GACACTGTTG	CAGAGAATGA	TGATGGCGGG	TTCAGTGAGG	1560
AATGGGAAGC	CCAGAGGGAC	AGTCATCTAG	GGCCTCATCG	CTCTACACCT	GAGTCACGAG	1620
CTGCTGTCCA	GGAACCTTCC	AGCAGTATCC	TCGCTGGTGA	AGACCCAGAG	GAAAGGGGAG	1680
TAAAACTTGG	ATTGGGAGAT	TTCATTTTCT	ACAGTGTTC	GGTTGGTAAA	GCCTCAGCAA	1740
CAGCCAGTGG	AGACTGGAAC	ACAACCATAG	CCTGTTTCGT	AGCCATATTA	ATTGGTTTGT	1800



GCCTTACATT ATTACTCCTT GCCATTTTCA AGAAAGCATT GCCAGCTCTT CCAATCTCCA	1860
TCACCTTTGG GCTTGTTTTT TACTTTGCCA CAGATTATCT TGTACAGCCT TTTATGGACC	1920
AATTAGCATT CCATCAATTT TATATCTAGC ATATTTGCGG TTAGAATCCC ATGGATGTTT	1980
CTTCTTTGAC TATAACCAA TCTGGGGAGG ACAAAGGTGA TTTTCCTGTG TCCACATCTA	2040
ACAAAGTCAA GATTCCCGGC TGGACTTTTG CAGCTTCCTT CCAAGTCTTC CTGACCACCT	2100
TGCACTATTG GACTTTGGAA GGAGGTGCCT ATAGAAAACG ATTTTGAACA TACTTCATCG	2160
CAGTGGACTG TGTCTCGGT GCAGAACTA CCAGATTGA GGGACGAGGT CAAGGAGATA	2220
TGATAGGCCC GGAAGTTGCT GTGCCCCATC AGCAGCTTGA CGCGTGGTCA CAGGACGATT	2280
TCACTGACAC TGCGAACTCT CAGGACTACC GGTACCAAG AGGTTAGGTG AAGTGGTTTA	2340
AACCAAACGG AACTCTTCAT CTTAACTAC ACGTTGAAAA TCAACCCAAT AATTCTGTAT	2400
TAAGTGAATT CTGAACTTT CAGGAGGTAC TGTGAGGAAG AGCAGGCACC AGCAGCAGAA	2460
TGGGGAATGG AGAGGTGGGC AGGGGTTCCT GCTTCCCTTT GATTTTTTGC TGCAGACTCA	2520
TCCTTTTTTAA ATGAGACTTG TTTTCCCCTC TCTTTGAGTC AAGTCAAATA TGTAGATGCC	2580
TTTGGCAATT CTTCTTCTCA AGCACTGACA CTCATTACCG TCTGTGATTG CCATTTCTTC	2640
CCAAGGCCAG TCTGAACCTG AGGTTGCTTT ATCCTAAAAG TTTTAACCTC AGGTTCCAAA	2700
TTCAGTAAAT TTTGGAAACA GTACAGCTAT TTCTCATCAA TTCTCTATCA TGTGGAAGTC	2760
AAATTTGGAT TTTCCACCAA ATTCTGAATT TGTAACATA CTTGTACGCT CACTTGCCCC	2820
AGATGCCTCC TCTGTCCTCA TTCTTCTCTC CCACACAAGC AGTCTTTTTT TACAGCCAGT	2880
AAGGCAGCTC TGTCGTGGTA GCAGATGGTC CCACTTATTC TAGGGTCTTA CTCTTTGTAT	2940
GATGAAAAGA ATGTGTTATG AATCGGTGCT GTCAGCCCTG CTGTCAGACC TTCTTCCACA	3000
GCAAATGAGA TGTATGCCCA AAGCGGTAGA ATTAAAGAAG AGTAAATGG CTGTTGAAGC	3060
AAAAAAAAA AAAAAAAAAA AAAAAAA	3087

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACCAAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTANAGGGAA	180

GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240
TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTTGG TGGAAATTAT	300
TGTACATCTT TTAAATCTG TGTAATTTTT TTTCAAGGAA GTGTTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC	480
CCTCATGNCC CTGKTGTTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC	540
TGTGATTTCA GTATATGGTA AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC	600
ACTGGAGTGT TTTCTTTCCT CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAATT AGCTATAGTA ACTTTTTCAT TTGAAGATTT	720
CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG	780
ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT	120
AATAGTGCTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCAG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCATCATG	CTTCACGGGG	GAGGCTGTGC	GGGAAGAATG	CTCCACACA	GNATAAAGAA	60
TGCTCCCGCA	CAGGATAGAG	AATGCCCCCG	CACAGCATAG	AGAAGCCCCC	GCACAGCATA	120
GAGAATGCCC	CCNCACAGCA	TAGAGAAGCC	CCCGCACAGC	ATAGAGAATG	CTCTTCACCT	180
CTGGGTTTTT	AACCAGCCAA	ACTAAATCA	CAGAGGSCMA	CACATCATTT	AAGATAGAAA	240
TTTCTGTATC	TTTTAATTTY	TTTCMAAGTA	GTTTTACTTA	TTTTCAGATT	CTATTTCTTT	300
ACTAGAATTA	AGGGATAAAA	TAACAATGTG	TGCATAATGA	ACCCTATGAA	ACMAACMMAA	360
GCTAGGTTTT	TTTCATAGST	CTTCTTCCAG	ATTGAATGAA	CGTCTGTTCT	AAAATTTAAC	420
CCCCCAGGGA	AATATTCAGT	TAACATATGTT	AAAAACCCAG	ACTTGTGATT	GAGTTTTGCC	480
TGAAAATGCT	TTCATAATTA	TGTGTGAATG	TGTGTC			516

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1726 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATCCCTCC	CCTTTTTAGA	CCATACAAGG	TAACCTCCGG	ACGTTGCCAT	GGCATCTGTA	60
AACTGTCATG	GTGTTGGCGG	GGAGTGTCTT	TTAGCATGCT	AATGTATTAT	AATTAGCGTA	120
TAGTGAGCAG	TGAGGATAAC	CAGAGGTCAC	TCTCCTCACC	ATCTTGTTTT	TGGTGGGTTT	180
TGGCCAGCTT	CTTTATTGCA	ACCAGTTTTA	TCAGCAAGAT	CTTTATGAGC	TGTATCTTGT	240
GCTGACTTCC	TATCTCATCC	CGNAACTAAG	AGTACCTAAC	CTCCTGCAAA	TTGMAGNCCA	300
GNAGGTCTTG	GNCTTATTTN	ACCCAGCCCC	TATTCAARAT	AGAGTNGYTC	TTGGNCCAAA	360
CGCCYCTGAC	ACAAGGATTT	TAAAGTCTTA	TTAATTAAGG	TAAGATAGKT	CCTTGSATAT	420
GTGGTCTGAA	ATCACAGAAA	GCTGAATTTG	GAAAAAGGTG	CTTGGASCTG	CAGCCAGTAA	480
ACAAGTTTTC	ATGCAGGTGT	CAGTATTTAA	GGTACATCTC	AAAGGATAAG	TACAATTGTG	540
TATGTTGGGA	TGAACAGAGA	GAATGGAGCA	ANCCAAGACC	CAGGTAAAAG	AGAGGACCTG	600
AATGCCTTCA	GTGAACAATG	ATAGATAATC	TAGACTTTTA	AACTGCATAC	TTCTGTACA	660
TTGTTTTTTC	TTGCTTCAGG	TTTTTAGAAC	TCATAGTGAC	GGGTCTGTTG	TTAATCCCAG	720

GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTTAC TGAAAATGTT TTTCTTGTGC	780
TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCCT	840
GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTTCTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT	1200
CATGTTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG	1260
ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCGCCCATTG NTCTTCTGCC TAGAATATTC TTTCCTTTNC TNACTTKGGN GGATTAAATT	1380
CCTGTCATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTTCC TTTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTTG GGACAAGGGA GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCCNGCT GNTGTGTNCT NCCCCACTG ANTAGGGTTA	1620
GACTGGACAG GCTTAACTA ATTCCAATTG GNTAATTTAA AGAGAATNAT GGGGTGAATG	1680
CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCACAGGC AAGATCTTCT CCTACCTTCC	60
CCCNNGGTGT AATACCAAGT ATTCNCCAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA	120
CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTTCACAC TACAGTAGCA CAGTTGAGTG	180
TTTGCCCTGG AGACCATATG ACCCATAGAG CTTAAAATAT TCAGTCTGGC TTTTACAGA	240
GATGTTTCTG ACTTTGTAA TAGAAAATCA ACCCAACTGG TTAAATAAT GCACATACTT	300
TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTACGTTT	360
ATCCAAGGAC TCAATCTCCT TCTTTCTTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG	420
TCCAGGCTGG AGCCCTASCC TTCATTTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC	480

ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA	540
AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT	600
CTKKNTGGCT GGGAAATATTG GCACCTGGAA TAAAAATGTT TTTCTGTGAA TGAGAAACAA	660
GGGGAAGATG GATATGTGAC ATTATCTTAA GACAACTCCA GTTGCAATTA CTCTGCAGAT	720
GAGAGGCACT AATTATAAGC CATATTACCT TTCTTCTGAC AACCCTTGT CAGCCNCGT	780
GGTTTCTGTG GCAGAATCTG GTTCYATAMC AAGTTCCTAA TAANCTGTAS CCNAAAAAAT	840
TTGATGAGGT ATTATAATTA TTTCAATATA AAGCACCCAC TAGATGGAGC CAGTGTCTGC	900
TTACATGTT AAGTCCTTCT TTCCATATGT TAGACATTTT CTTTGAAGCA ATTTTAGAGT	960
GTAGCTGTTT TTCTCAGGTT AAAAATTCTT AGCTAGGATT GGTGAGTTGG GGAAAAGTGA	1020
CTTATAAGAT NCGAATTGAA TTAAGAAAAA GAAAATTCTG TGTGAGGT GGTAATGTGG	1080
KTGGTGATCT YCATTAACAC TGANCTAGGG CTTTKGKGT TGKTTTATTG TAGAATCTAT	1140
ACCCCATTC AAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT	1200
GCTGCCATCA TGATCAGNGT CATTGTWGT ATGACTANNC TCCTGGTGGT TCWGTATAAA	1260
TACAGGTGCT ATAAGGTGAG CATGAGACAC AGATCTTGN TTTCCACCCT GTTCTTCTTA	1320
TGGTTGGGTA TTCTTGTCAC AGTAACTTAA CTGATCTAGG AAAGAAAAA TGTTTTGTCT	1380
TCTAGAGATA AGTTAATTTT TAGTTTTCTT CCTCCTCACT GTGGAACATT CAAAAAATAC	1440
AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT	1500
TGGGCCCAGG AGTTCACAAG CAGCTTGGGC AACGTAGCAA GACCCTGCCT CTATTAAAGA	1560
AAACAAAAA CAAATATTGG AAGTATTTTA TATGCATGGA ATCTATATGT CATGAAAAA	1620
TTAGTGTAAT ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT	1680
TTGGGATTC AATGCCTTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAA	1740
AGTTGTAAC TAAAAATAAA CATTTCCATA TAATAGCACA ATCTAAGTGG GTTTTGN	1800
GTTTGTGTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT	1860
GGCACGATTT TGGCTCACTG CAG	1883

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 823 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGGAGTGGA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCNG GGACATAGTG	60
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GTACACANCT	GTAATGCTCA	NCACTKATGG	GGAGTACTGA	AGGNGGNSGG	ATCACTTGNG	120
GGTCNGGAAT	NTGAGANCAG	CCTGGGCAAN	ATGGCGAAAC	CCTGTCTCTA	CTAAAAATAG	180
CCANAAWNWA	GCCTAGCGTG	GTGGCGCRCA	CGCGTGGTTC	CACCTACTCA	GGAGGCNTAA	240
GCACGAGNAN	TNCTTGAACC	CAGGAGGCAG	AGGNTGTGGT	GARCTGAGAT	CGTGCCACTG	300
CACTCCAGTC	TGGGCGACMA	AGTGAGACCC	TGTCTCCNNN	AAGAAAAAAA	AAATCTGTAC	360
TTTTTAAGGG	TTGTGGGACC	TGTTAATTAT	ATTGAAATGC	TTCTYTTCTA	GGTCATCCAT	420
GCCTGGCTTA	TTATATCATC	TCTATTGTTG	CTGCTCTTTT	TTACATTCAT	TTACTTGGGG	480
TAAGTTGTGA	AATTTGGGGT	CTGTCTTTCA	GAATTAACTA	CCTNNGTGCT	GTGTAGCTAT	540
CATTTAAAGC	CATGTACTTT	GNTGATGAAT	TACTCTGAAG	TTTTAATTGT	NTCCACATAT	600
AGGTCATACT	TGGTATATAA	AAGACTAGNC	AGTATTACTA	ATTGAGACAT	TCTTCTGTNG	660
CTCCTNGCTT	ATAATAAGTA	GAAGTAAAAG	NAACTTAAGA	CTACAGTTAA	TTCTAAGCCT	720
TTGGGGAAGG	ATTATATAGC	CTTCTAGTAG	GAAGTCTTGT	GCNATCAGAA	TGTTTNTAAA	780
GAAAGGGTNT	CAAGGAATNG	TATAAANACC	AAAAATAATT	GAT		823

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 736 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTTCCCA	TCTTCTCCAC	AGAGTTTGTG	CCTTACATTA	TTACTCCTTG	CCATTTTCAA	60
GAAAGCATTG	TCAGCTCTTC	CAATCTCCAT	CACCTTTGGG	CTTGTTTTCT	ACTTTGCCAC	120
AGATTATCTT	GTACAGCCTT	TTATGGACCA	ATTAGCATTC	CATCAATTTT	ATATCTAGCA	180
TATTTGCGGT	TAGAATCCCA	TGGATGTTTC	TTCTTTGACT	ATAACAAAAT	CTGGGGAGGA	240
CAAAGGTGAT	TTCCTGTGTC	CACATCTAAC	AAATCAAGAT	CCCCGGCTGG	ACTTTTGGAG	300
GTTCCCTTCCA	AGTCTTCCTG	ACCACCTTGC	ACTATTGGAC	TTTGGGAAGGA	GGTGCCTATA	360
GAAAACGATT	TTGAACATAC	TTCATCGCAG	TGGACTGTGT	CCTCGGTGCA	GAAACTACCA	420
GATTTGAGGG	ACGAGGTCAA	GGAGATATGA	TAGGCCCGGA	AGTTGCTGTG	CCCCATCAGC	480
AGCTTGACGC	GTGGTCACAG	GACGATTTTC	ACTGACACTG	CGAACTCTCA	GGACTACCGT	540
TACCAAGAGG	TTAGGTGAAG	TGGTTTAAAC	CAAACGGAAC	TCTTCATCTT	AAACTACACG	600
TTGAAAATCA	ACCCAATAAT	TCTGTATTAA	CTGAATTCTG	AACTTTTCAG	GAGGTACTGT	660
GAGGAAGAGC	AGGCACCACC	AGCAGAATGG	GGAATGGAGA	GGTGGGCAGG	GGTTCAGCT	720

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNNWGTA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACA TTCCNTTAAG GATTACTCAA GCYCCCCTTT TGSTGKNWAA TCAGANNGTC	360
ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTT CTACTTATTG	420
CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA	480
TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT	540
ACTAGGATTT AACTAACAAT GGATGACCTG GTGAAATCCT ATTTGAGACC TAATCTGGGA	600
GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT	660
GAAAGAAAGG TTTGTTTCTG CTTAATGTAA TCTATGGAAG TGTTTTTTTAT AACAGTATAA	720
TTGTAGTGCA CAAAGTTCTG TTTTCTTTT CCTTTTCAGA ACCTCAAGAG GCTTTGTTTT	780
CTGTGAAACA GTATTTCTAT ACAGTNTGCT CCAANTGNAC AGAGTTACCT GCACNNCGTT	840
GTCCNTACTT CCAGAATGCA CAGATGTCTG AGGACAACCA CCTGAGCAAT ACT	893

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGAAAATA CTTTNGGGCA CATGAGAATC ACATGAGAAC AAGCTGATGC ATAATTCCTC	60
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CTGTGATGGA ATGTAATAGT AATTTAACAG TGTCTTTTCT TTTTAACTGC CTCAAGGATA	120
CAGCAAAAATA AAACAAAAGC AATATGAAGG CTGAGAATAG GTATCAGATT ATCATAAAAA	180
GTATAGATCA AAAGGAATCT GGTCKTNAGG TTGGCGCAGC AGCCTCTAGA AGCGACNAGG	240
GAGACTTTTA GAACTACCAT TCTCCTCTAT AAGTGGATCC NANGCCCAGG RAAACTTGAT	300
ATTGAGNACA ATGGCCTTAC TGAAATAACC TGTGATCCAC TCGGNCTCAT CATCTCCACC	360
ACCACCATAA ATTTGATGAG TNCCTATAAT ATTCCANCCA GNGGAAATAC CTGGRAGGTT	420
ACTGAAAGGC NACNATCAGA CNAATAATAA GNATACCGTA GGTAATTCT ACAGT	475

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTTCTCNAGA TCTCTTCAAA ATTCATTNTG CGCTATAGGA GCTGGGATTA CCGCGGGTGC	60
TGGAACCAGA CTTGCNCTCC AATGGATCCT CCANACNGGA NGGGGGGTGG ACTCACACCA	120
TTTACAGGGG GCTCGTAAAG AATCCTGTTT TGANTATTNT NCCGTCAATT ACCNCCCCAA	180

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 457 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGTAACMA CMAAACCYCA AACTCCTGNA AGAANATGGT TACTTATNGA TNCCATTTNC	60
TTTTTNCACT CTCAGACATA AATATAAACM MANTTTCTAC TGTGGRAAAA CATCTNCAGG	120
GGNCNTTTAN CCATGATCTC TAGNACNANG GGCTNGTGGN TNGTTTTAAT GTCTCTAAGC	180
NACTNGACTA GTTTCTCTTN CACTGAGNAA ACTGCNACAA GTNNTTNCTN CTGNATCTGN	240
ACTGNAATGC TAAGTTNCAA GTNCCAATGA GCTNGTGANT TANYCTTTAT TTNAMCNAAA	300
GTNNTTAATC ANCCNCAGTG TTACTTTGNA AAGCTNCTCC CTGGACAGGC GGCCCNACTT	360
CTAATGTTAT GAATGGGCTG GAGNANCCTC NACNTGAGTT TNNWAAGGNT CAACANCCAA	420
TRGNAANTGT AMCCGACTCT AAATTCCAAC CNATAAT	457



(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTGTGCTA GGTAGTGTAC TAATCATTCA GTTTATCTCA TTTAATCTNN ATGNAACTCT	60
AAGTCATTCG CTNTGANCNA CACATAACAG ATCTCGCAAC TGNAGTTTAG CGAGGCCAGT	120
TAATTTKCCA AAGNTCATAA TNCTAAGNAG TTCTAGNATG GAGATTCMAA GTCCNACTGT	180
TTAGTCAAGA GACCCTACTG TTAAC TAGTA CCTTTACT ACTAACTGGG TAANCCATAA	240
NCAATTAATG ATAAAGATTG AGATTACTKC CACATTCTCA CTGGTTATAA ATTAAACNT	300
CAAATAAAAA NTCTTGGCAC TTCTATGGTA ATATTTTAT TAGGATAAAC TTTCAAGNAG	360
TGGATNCTAG GTG	373

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCACACTGN TGGGCCATGG AAGCCATGAG TGTACCACAT GGCCCTGTCC CACTGGCCAC	60
AGTNGATTGG TTGGNTCGGG AGTAGTCACC TGATTCAAGN TGGGCCAATC AGATCCTACC	120
TCCANGGGGT TNGGAATTAG AAAACAGTGA CCCTAGYTAG TNTAGGCNAC TTGAACTGGA	180
GGGCCCATAC ATTCAGGAGC CTTATGGGGC CATGTACACA TGGAAGCAGG AAGANTGAAG	240
GAGGGAGAAG TAGAGGCCAG AAACCCACCT GGGTTCCTGT TTCCAATGN TAAGTCCCTG	300
CCATGTYCCT GCTCTTCCTG TGGTTNGGAT CTTCAAAGGT TGCTCAAATT NGGGGCAGTG	360
GCCCTGGCAG CTTTTCAAAT CCTYCCCATT TTTATTGAAG CTGAAAGACC CTTGACTAGA	420
AC	422

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATTGTTATTT TTCGTCAC TA CCTCCCCGGG TCGGGAGTGG GTAATTTGCG CGCCTGCTGC	60
CTTCCTTGGA TGTGGTAGCC GTTTCTCAGG CTCCCTCTCC GGAATCGAAC CCTGATTCCC	120
CGTCACCCGT GGTCAACATG GTTAGGCACG GCGACTACCA TCGAAAGTTA ATAGGGCAGA	180
TCTCGAGAAT TCTCGAGATC TCCNTCMAAT TATTACTTCA NTTKCGGTAG TGATCAGNAC	240
NAGGCAGTTC TATTGATTTC TCTCCTTTCA TTCTGAGTTT CTCCATAAAT TAATTGGACC	300
TAATCATGTT TKNAATCCTG TCTTTTAGGG GGNANTTGNA CTNTCAAGTG TTTAAAGGGA	360
GGGNCGGAGN ATGATTNTGG ATTGGAGTGA GAGCA	395

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGANTTTCT GGGTNAAAAG GACCTNANAC ATAATATAGT GGA CTTNCAA TAAACACTTA	60
CCAAATGGAN AAATGAACCC CTGGTCACCC CGATCTCACT AGTNCCTNCC CTGAAACCCG	120
ANANATCTGA GTCCTTTTCT CCTTTACTAA CCCTTNCTCC AATCCTGCTC ATGGGAATTA	180
ANGNTGTAAA ATANGCCTGG GGNACCTCGG RCCTCTNCCC TGGGNTCTGT GGGTGGGAGN	240
ACTGTGGAAG CCGTWTCAAT CGCCCCCACC TATGAGAGCC TTTCTNCAGG GCCAGCCATG	300
AACGTCCCCC ATGTNATCAG NATCTNCAGG CTACTGCTGT CCTTCYTGGA TWTTTAACCT	360
GGRGGCGGGC CAGGGACAGA AAARGGAGGT GGCAAGATCC TTGAACAAAA GGAGCTATAA	420
AAGGGCGTTG GGGGAAGCAA GGCAAACGGC AGATTAAACA AGCAGGCACC TCAAGGAAAC	480
GTGACGC	487

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGAGATCT GGCCCATCAT TTAGTTTTAT NGCTTGNAGT NTNTAGNAGA TAAAACATCC	60
ACGTGGATCT NCTCTTAGAG AAATCAANTA CTTTAGGNAT NTGATAGTCA GAGANTGGNT	120

ATCAAATNGA AAGGNATNTN GGTNGANCAG TTAGTTNGYN CCNTTNGNNG AGACCACTGG	180
GNTGTNGASA CCAGATTCKM GGGTNCNAAT CTTANGGTAA TCTNAGAGCC AACACATGGG	240
TCATNTTATS CCCCAAACCT AGCCACATCT BGTGGGGYTA TGGNGTCACC CCAAGAGCAG	300
GAGGAGCATG GNTGGATGGA AATCCATCTC CACCACTGGA ACCCCAATT CTGAATGNAT	360
CACCTGTTAG AGTTTCTTGT YCATAAAATA GCAGGGAATT TAGGAATTTA GTTTTTTTTT	420
AATAGTTTGG GCCTTTTATC CACACTCTCA GGAGCTTAGG ATACTTTTCT CCTTCAGCTC	480
ACTCTGAAAC TCCCTCTGGA	500

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 406 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCGAGATCTG TGGTAGTNAC ATGATATTCT GGCAMCTACT TTCATTATCA CCTTTATTAA	60
AATAAATTTA AAGAAAAATG GCAGTATGTT TCTGTGRAGN CCACGAGTAC TCATTTTAAA	120
GGACTCMAGA GTTNCAGRNA AGTAAAAAGR AAAGAGTAAA ATCATTTTCT AANTYTYWYY	180
TTCCAGAAAT AACGATGTTG AGCATTAAGT GGACTTCATT TCATACTCTT TCMMAGNTTA	240
TGTAGGCATA WAWATGTGTG TGTATATACA TATATATGGG TACATCCTTA GAGAAGTTGG	300
CTGGCTAGAT AGACACACNT NAAAAATGGR ATCATACTCT AATKCCATTT NNANTTTANA	360
AAATACATAT TCAGANCCNC TGTNCTTATA NACAGAGTAA NTGAAA	406

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACCCAGTAA AACTTATCTC ATGAGCATAA GGCTGAATGG GATTGACAGC CTACAGAACC	60
CGGATTTTAT CATGAGGGCA TTAGTGGGGG TTGGGGGTTA GGTACTGAAA GTTTAAGGAG	120
GTGAAAGGAA AGCAACTTGT GCCTTACAGG GTCAAGCTAG GTCAAGGAAA TTCCCAGGAG	180
CGTGTGGAAG CTCTCTACCT GATAGGTGAG CTCAAGCTTA TGACCGCCCA AGCTTCTCCC	240
CAAGCTTCCC TTCCACTGCT TCCTCTTGAT TGAATTCCAC AGCAAGGTC	289

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 367 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATCAGGAT TTACTGAGTA AAAATCTCAG GTNTTAACCA TGCCCCTAAA ATGTGCTATN	60
CCAAAGAGGA ACAGGTTACT TGGGAGGAAA AAAGCTGCCT GGGNAACTCC CCNCAAATGT	120
TTATTTTAAA TAAAAATGGT NGATGGAAAT ATTTTNTAAA AGAACTTGGG GTNTAATATG	180
GNATACTGCC CATCAAACAA AAAAGGAAAT AAAACTTCNT TCCCATTAT AATAAGTTNC	240
CCACCCTTTA CTATCAAGAT TACAACCTAT TGACCTTTTA TGCTNGCTNG GTTTTTTTGG	300
GACTGCCTAA TCCAATGTTT AAATTTTCTA NGTCTGNATT TCAATGTGGG TAGGAGTNAT	360
TTTTCAA	367

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 425 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGTATCTGA CAGGTAAGAT TGCTTTTTTA AGTTGTTTTA AATGCATTAC ATGACTGAGA	60
AAAGAAAAAT GCACATTTTA TTGTTGCAGT TTAAAATTTT ATTTNGNGTG AAATAAACG	120
TGAAACAAAA GGGATAAATG TGTTTTGNTT TTGTTTTGGT TTTACCTGTT TGGGGTATTT	180
TTTTCTGAGT TTGTGTAGAA ACCCGTGTGG NTACACTGGG TAATCTTGTC AGGGNTACMA	240
AMCTTGGGTC TTGANTTTGG TTANTTGGNT TTANTTGGTG NACCCATGTA CTTGCTCTTC	300
CNTCCCAGAA ACATAGCTTG GTAGGCNAGG GTTAANCCAG TGTCGGCGAN CCCATGTCCC	360
TANCACAGCA TCTTGTAAGT TTAATGCACA ATCGTTCCNT CCCAGGATGG ANTTATCATT	420
ATAAA	425

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 2377 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGAGGCGCA	GGAGCCACAA	ATAAAGCAAG	AGCCAGAATC	AGAAGNGGAG	GAAGAAGAAA	60
AGCAAGAAAA	AGRAGRAANA	CGAGAAGAAC	CCATGGRAGA	GGAAGAGGAN	CCAGANCMMA	120
AGCCTTGTCT	GAAACCTACT	CTGAGGCCCA	TCAGCTCTGC	TCCATCTGTT	TCCTCTGCCA	180
GTGGNAATGC	NACACCTAAC	ACTCCTGGGG	ATGAGTCTCC	CTGTGGTATT	ATTATTCCTC	240
ATGRAAACTC	ACCAGATCAA	CAGCAACCTG	AGGAGCATAG	GCCMAAAATA	GGACTAAGTC	300
TTAAACTGGG	TGCTTCCAAT	AGTCCTGGTC	AGCCTAATTC	TGTGAAGAGA	AAGAACTAC	360
CTGTAGATAG	TGTCTTTAAC	AAATTTGAGG	ATGAAGACAG	TGATGACGTA	CCCCGAAAAA	420
GGAAACTGGT	TCCCTTGGAT	TATGGTGAAG	ATGATAAAAA	TNCAACCAAA	GGCACTGTAA	480
ACACTGAAGA	AAAGCGTAAA	CACATTAAGA	GTCTCATTGA	GAAAATCCCT	ACAGCCAAAC	540
CTGAGCTCTT	CGCTTATCCC	CTGGATTGGT	CTATTGTGGA	TTCTATACTG	ATGGAACGTC	600
GAATTAGACC	ATGGATTAAT	AAGAAAATCA	TAGAATATAT	AGGTGAAGAA	GAAGCTACAT	660
TAGTTGATTT	NGTTTGTCT	AAGGTTATGG	CTCATAGTNC	ACCCAGAGC	ATTTTAGATG	720
ATGTTGCCAT	GGTACTTGAT	GAAGAAGCAG	AAGTTTTTAT	AGTCAAATG	TGGAGATTAT	780
TGATATATGA	AACAGAAGCC	AAGAAAATTG	GTCTTGTGAA	GTAAACTTTT	TTATATTTAG	840
AGTTCCATTT	CAGATTTCTT	CTTTGCCACC	CTTTTAAGGA	CTTKGAATTT	TTCTTTGTCT	900
TKGAAGACAT	TGTGAGATCT	GTAATTTTTT	TTTTTTGTAG	AAAATGTGAA	TTTTTTGGTC	960
CTCTAATTTG	TTGTTGCCCT	GTGTACTCCC	TTGGTTGTAA	AGTCATCTGA	ATCCTTGGTT	1020
CTCTTTATAC	TCACCAGGTA	CAAATTACTG	GTATGTTTTA	TAAGCCGCAG	CTACTGTACA	1080
CAGCCTATCT	GATATAATCT	TGTTCTGCTG	ATTTGTTTCT	TGTAAATATT	AAAACGACTC	1140
CCCAATTATT	TTGCAGAATT	GCACTTAATA	TTGAAATGTA	CTGTATAGGA	ACCAACATGA	1200
ACAATTTTAA	TTGAAAACAC	CAGTCATCAA	CTATTACCAC	CCCCACTCTC	TTTTCATCAG	1260
AAATGGCAAG	CCCTTGTGAA	GGCATGGAGT	TTAAAATTGG	AATGCAAAAA	TTAGCAGACA	1320
ATCCATTCCCT	ACTGTATTTT	TGTATGAATG	TGTTTGTGAA	TGTATGTGTA	AAAGTCTTTC	1380
TTTTCCCTAA	TTTGCTTTGG	TGGGGTCCTT	AAAACATTTT	CCAATAAAG	AATAGAATTG	1440
TAAAGGAAAA	GTGGTACTGT	TCCAACCTGA	AATGTCTGTT	ATAATTAGGT	TATTAGTTTC	1500
CCAGAGCATG	GTGTTCTCGT	GTCGTGAGCA	ATGTGGGTTG	CTAACTGTAT	GGGGTTTTCT	1560
TATTAATAAG	ATGGCTGCTT	CAGCTTCTCT	TTTAAAGGAA	TGTGGATCAT	AGTGATTTTT	1620
CCTTTTAATT	TTATTGCTCA	GAAATGAGGC	ATATCCCTAA	AAATCTCGGA	GAGCTGTATT	1680
TAATGCATTT	TTGCACTAAT	TGGTCCTTAG	TTAATTCTA	TTGTATCTGT	TTATTTAACA	1740
AAAAATTCAT	CATATCAAAA	AGTGTAAGTG	AAAACCCCTT	TTAAACAAA	ACAAAAAAT	1800
GAAATAAAAT	TAGGCAAAAT	GACAGACAGT	GAGAGTTTTA	CAAACATGAT	AGGTATTCTG	1860

CTCGGCAATT TGTAAGTTTA CATGTTATTT AAGGATAAAG GTAAATCATT CAAGGCAGTT	1920
ACCAACCACT AACTATTTGT TTTCATTTTT GTCTTGTAGA AGGTTTATAT CTTGTTTTAC	1980
CTTGGCTCAT TAGTGTTTAA AAATGTACTG ATGATGTGCT TAGAGAAATT CCTGGGGCTT	2040
TCTTCGTTGT AGATCAGAAT TTCACCAGGG AGTAAAATTA CCTGAAAACG TAAGAAGTTT	2100
TAAACAGCTT TCCACACAAA TTAGATGCAA CTGTTCCCAT GTCTGAGGTA CTTATTTAAA	2160
AGAAAGGTAA AGATTGGCCT GTTAGAAAAA GCATAATGTG AGCTTTGGAT TACTGGATTT	2220
TTTTTTTTTT TAAACACACC TGGAGAGGAC ATTTGAAAAC ACTGTTCTTA CCCTCGAACC	2280
CTGATGTGGT TCCATTATGT AAATATTTCA AATATTAAAA ATGTATATAT TTGAAAAAAA	2340
AAAAAAAAAA AAAATTCCTG CGGCCGCAAG GGAATTC	2377

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 489 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATTGGAGCTC CACCGCGGTG GCGGCCGCTC TAGNAACTAG TGGATCCCCC GGGCTGCAGG	60
AATTCTCGAG ATCTCCCCCA AGTAAATGAA TGAAAAAAG AACAGCAACA ATAGAGATGA	120
TATAATAAGC CAGGCATGGA TGACCTTATA GCACCCTGTA TTTATACAGA ACCACCAGGA	180
GGATAGTCAT GACAACNATG ACACTGATCA TGATNCCAGC ATTCAGAATT GAGTNCAGGG	240
CTCTCTGGCC CACAGTCTCG GTATCTTCTG TGNATGGGGT ATAGATTARC TGTCCATCCT	300
TCCGGGNATA AAANCTGACT GACTTAATGG TANCCACGAC CACCACCCAT KCAGAGAGTC	360
ACAGGGACMA AAGAGCATGA TCAACATGCT TGGCNCCATA TTTCAATNTC ANCTCCTCAT	420
CTTCTCCTC ATCTTNCTCC ACCACCTNCC GGGAGTTAAC CCTGGGGTCG TCCATTAGAT	480
AATGGCTCA	489

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2307 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGTGCTTC AGTGTGGCTG ACACAGCAGC ATGGTCTTGA CAAGTTTTCT TCATCCTACC	60
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ACAAAATCCC	AGTTGGTAAT	AGAGACTTTA	CTCCTACCTA	TCAAAACCAC	AAAATGTCCC	120
ATTAGGGGGG	GACATGTTGT	ACATGTTAGG	ATCATTCAAA	TAACCAAGAT	TATAAGGTGA	180
GGAAAGATGC	CCCTAACTGA	TTCTTTTGTC	TCTCATCTTG	TTGGTTCCAG	GGACCGAGTG	240
GGGTCAATCT	TCTGGTSSTG	CCTCTCCAGG	TCTCTTCCAG	GCCGGTCATA	GACGTACTCC	300
CTCTGAGGCC	GACCGATGGT	TAGAAGAGGT	GTCTAAGAGC	GTCCGGGCTC	AGCAGCCCCA	360
GGCCTCAGCT	GCTCCTCTGC	AGCCAGTTCT	CCAGCCTCCT	CCACCCACTG	CCATCTCCCA	420
GCCAGCATCA	CCTTTCCAAG	GGAATGCATT	CCTCACCTCT	CAGCCTGTGC	CAGTGGGTGT	480
GGTCCCAGCC	CTGCAACCAG	CCTTTGTCCC	TGCCCAGTCC	TATCCTGTGG	CCAATGGAAT	540
GCCCTATCCA	GCCCCTAATG	TGCCTGTGGT	GGGCATCACT	CCCTCCCAGA	TGGTGGCCAA	600
CGTWTTTGGC	ACTGCAGGCC	ACCCTCAGGC	TGCCCATCCC	CATCAGTCAC	CCAGCCTGGT	660
CAGGCAGCAG	ACATTCCCTC	ACTACGAGGC	AAGCAGTGCT	ACCACCAGTC	CCTTCTTTAA	720
GCCTCCTGCT	CAGCACCTCA	ACGGTTCTGC	AGCTTTCAAT	GGTGTAGATG	ATGGCAGGTT	780
GGCCTCAGCA	GACAGGCATA	CAGAGGTTCC	TACAGGCACC	TGCCCAGTGG	ATCCTTTTGA	840
AGCCCAGTGG	GCTGCATTAG	AAAATAAGTC	CAAGCAGCGT	ACTAATCCCT	CCCCTACCAA	900
CCCTTTCTCC	AGTGACTION	AGAAGACGTT	TGAAATTGAA	CTTTAAGCAA	TCATTATGGC	960
TATGTATCTT	GTCCATACCA	GACAGGGAGC	AGGGGGTAGC	GGTCAAAGGA	GCMAAACAGA	1020
YTTTGTCTCC	TGATTAGTAC	TCTTTTCACT	AATCCCAAAG	GTCCCAAGGA	ACAAGTCCAG	1080
GCCCAGAGTA	CTGTGAGGGG	TGATTTTGAA	AGACATGGGA	AAAAGCATTC	CTAGAGAAAA	1140
GCTGCCTTGC	AATTAGGCTA	AAGAAGTCAA	GGAAATGTTG	CTTTCTGTAC	TCCCTCTTCC	1200
CTTACCCCTT	TACAAATCTC	TGGCAACAGA	GAGGCAAAGT	ATCTGAACAA	GAATCTATAT	1260
TCCAAGCACA	TTTACTGAAA	TGTAAACAC	AACAGGAAGC	AAAGCAATGT	CCCTTTGTTT	1320
TTCAGGCCAT	TCACCTGCCT	CCTGTGAGTA	GTGGCCTGTA	TTAGAGATCA	AGAAGAGTGG	1380
TTTGTGCTCA	GGCTGGGAAC	AGAGAGGCAC	GCTATGCTGC	CAGAATTCCC	AGGAGGGCAT	1440
ATCAGCAACT	GCCCAGCAGA	GCTATATTTT	GGGGGAGAAG	TTGAGCTTCC	ATTTTGAGTA	1500
ACAGAATAAA	TATTATATAT	ATCAAAAGCC	AAAATCTTTA	TTTTTATGCA	TTTAGAATAT	1560
TTTAAATAGT	TCTCAGATAT	TAAGAAGTTG	TATGAGTTGT	AAGTAATCTT	GCCAAAGGTA	1620
AAGGGGCTAG	TTGTAAGAAA	TTGTACATRA	GATTGATTTA	TCATTGATGC	CTACTGAAAT	1680
AAAAAGAGGA	AAGGCTGGAA	GCATGCAGAC	AGGATCCCTA	GCTTGTTTTT	TGTCAGTCAT	1740
TCATTGTAAG	TAGCACATTG	CAACAACAAT	CATGCTTATG	ACCAATACAG	TCACTAGGTT	1800
GTAGTTTTTT	TTAAATAAAG	GAAAAGCAGT	ATTGTCCTGG	TTTTTAAACCT	ATGATGGAAT	1860
TCTAATGTCA	TTATTTTAAT	GGAATCAATC	GAAATATGCT	CTATAGAGAA	TATATCTTTT	1920
ATATATTGCT	GCAGTTTCCT	TATGTTAATC	CTTTAACACT	AAGGTAACAT	GACATAATCA	1980

TACCATAGAA	GGGAACACAG	GTTACCATAT	TGGTTTGTAA	TATGGGTCTT	GGTGGGTTTT	2040
GTTTTATCCT	TTAAATTTTG	TTCCCATGAG	TTTTGTGGGG	ATGGGGATTC	TGGTTTTATT	2100
AGCTTTGTGT	GTGTCCTCTT	CCCCCAAACC	CCCTTTTGGT	GAGAACATCC	CCTTGACAGT	2160
TGCAGCCTCT	TGACCTCGGA	TAACAATAAG	AGAGCTCATC	TCATTTTTAC	TTTTGAACGT	2220
TGGCGCTTAC	AATCAAATGT	AAGTTATATA	TATTTGTACT	GATGAAAATT	TATAATCTGC	2280
TTTAACAAAA	ATAAATGTTC	ATGGTAG				2307

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 343 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCAGCTATT	TACATGGCCT	CACAGGCATC	AGCTGAAAAG	AGGACCCMAA	AAGAAATTGG	60
AGATATTGCT	GGTGTGCTG	ATGTTACAAT	CAGRCAGTTC	TATAGACTGA	TCTATCCTCG	120
AGCCCCAGAT	CTGTTCCCTA	CAGACTTCMA	ATTKGACACC	CCAGTGGACA	AACTACCACA	180
GCTATAAATT	GAGGCAGYTA	ACGTCMAATT	CTTGANNACM	AACTTKNCC	TGTTGTACAT	240
AGCCTATACM	AAATGCTGGG	TTGAGCCTTT	CATAAGGNAA	AACMNAAGAC	ATGGNTACGC	300
ATTCCAGGGC	TKGANTACTT	ATTGCTTGGC	ATTCTTGAT	GTA		343

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAGGGCTAA	CCAGCCACTG	CACCAAATT	AGTCCTTACA	TTATAATACT	CTGGCCATTG	60
GAAGAGAAAA	ATGGGAAAAT	TCAACAATTT	GAAAGACTAT	GATCCCTCTG	GCTCATGATC	120
TACTGACCAG	AATGAAGTCC	TGAAGGATTT	CCTTCTGTTA	TGTTATCTAC	CCAGCTAATC	180
TCAAACAAGA	GGAGCTGGAA	AGAACAAAGC	CCCATGAAGC	TACCCCTAGA	CCCAGAAAGC	240
CAAGAACAGG	GCCAAGAAAA	TGAACAGCAG	ACAAGCCTGA	AATAGAAGTG	GNACAGACAT	300
GTGGNAAGAC	CAAGTACACC	CAGTTNGGTG	GTAAAGATTC	CGATATCAAG	CTTATCGATA	360
CCG						363



(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 362 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTACATGGT TTCTTGNCCA CCCASCCAC CTTTCCCCAT CTCTACCGGY TGATAGTCTC	60
TCAGNTAGTA GACCTTTTCT NGTTTAGRCA GGGCCACNTT TTTAAAACT CCAGACGGGT	120
ACCTTCCATG TKGMAGGCGA CGTGGCCCTG GATCACTCAA CTGANTGTCA TNKGANTGGT	180
GCCCCCAGAG TGAGGACAAT GGTGNAGCCC TCCTAAGGCC CTNCCTGAGT GTCCCTCCTT	240
CATGAAGATG ATTCTGAGGN TTCCCAGGCC TNCACCCTTC TTKGAAARCC CATAGNAGTT	300
CATATGNACT NCTCTNCTAT GCTCACCAAA CTCTNCCTTC ATCATACTTG GGGGATGTGT	360
GT	362

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 475 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCATGTAA TTACAGTTAC GATATATGAA ACGTACAAAA TATTATGAGT ATATAATATG	60
GGGAGACTTA ATCTAGTTTG GGGGATCAGG GCACATTTCT CTAAGAAAGT GACATTTGAA	120
TTGAGCTCTG AAGGATAAAT AGACATTACC CAGAAGAATA AAATGATGGG GAAGAAGGAG	180
GACATTTTCC GTAGATTTCC AGTGGCCCN CTTGATCCCT TATCCACTCA TCACTNAGGA	240
GGATATTAAA TKCTATAGAA ATGGRAGRAA GACMMAAAGA GACCCTNATA TCTCGAGAGG	300
ATCCAGCMAA ATTCCAAGAG ACACAACAWT AAGAACTNG GAAGGAAGAG AAAAGGCMMN	360
NNAGGNAAAA GAAAGACAAG GAAATTNWN NAGNACGGAG AGAAAGAGAG AGGGAGCGTN	420
NAAGGGNACG AGAAAGGCGA GNACGGGGAC GAGAAAGGN AAGAGNACGT AAACG	475

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 346 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGAAATAAAT GAGATCTCAG TGGTGGTATG GATTGGACTG ATCTCTGTAA CTGTGTNTGG	60
AAAAAGGACC GGAAATGAA AGCCAGATCC CAGTAAGGGG TAGAGAGGGG CCAAGAGAAC	120
TGAACATCTG GGCTGCCGGA GAAATCAAAG TCTAGGAAGT AAGAGGTAAG AGTGTACTAC	180
AGGGGACATA CCCCAATCTC TTGGTTCCCT CCCTCTNCCT TCCTCTCCCA GAGACCCAGG	240
TCCCTGGGAC TATNTTGGAT CTGTCTCTGA AGCTGAAAAA CAAAAGGCAG AGGAGACAGT	300
CGGNTCTAAG TGACCAATCT CAAGCCAGCT TGGTCAGAAN TCCTAA	346

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 433 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAATCCAGTG CAGGCAACAT TATGTGGAAA TAGAAACAGG GCTCCTGCTA GGAGATTGAN	60
ATTCTGGCTT TCCTTTGGAA CCCCTCACTG ACTCATCGCC CCTGAANCAG GANCCANCAG	120
GTNCCAAGGC TCCCCTGCTC CTNTCCCTNC CCCAGGGCGA GATAGGAARC CGGAARCCTG	180
GGCAGGCTGA RCCCANCCGA CTGGAACCAG GGNAGANCCT GTGGGTGGGT GGNAGGGAGG	240
GAAGGAGGCC AGATTCCTCC AGAACTGGGG RAGAGAACAG GTTTTGAAG TTGGGGGAGG	300
GTTTGGGTTT CACAGTGATG GTTTCATGAN ACCCTGGAGG GTTNCACACT CCTGGTKCAN	360
TTTTGNTANT CGTNCTTTGA ANACARNCCG CTTCTTTCA ACCCTCCNCN TAAAAAGTTT	420
TGATNTTTTA AGG	433

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 350 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCAAGAGCC CCCAGTTTAT GNTAACTCTC ATGACAAACA CAATTTTAGT ACCTCTCACT	60
ACCAACTATC CAGGAACCAG GANTCACCTA TTACTACGGT TCCAGCAGAA TGGGAATCCC	120

ATTCTCGGAT ATCCAGGGTA AATCCCTGAC CATGTGAGAG GAATCCTAGT GCCCCAACAA	180
CCTCACCCCC TGA CTCCTCC TCAANGGCTC TGCCAAGTCA ACAAAAAAAT CCTCTACATT	240
TACACTATCT GTAAAGCCAA AGACCAGCGT CAACCTAAAT GTCCATCAAT AAGGGAATGG	300
TTGGATAAGT AAAAATTATG CAGCTGTAGG AAGGAATGAA GAATGTCTAT	350

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 512 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAGGGAACA AAAGCTGGTA CCGGGCCCCC CCTCGAGGTC GACGGTATCG ATAAGCTGGA	60
TATCGAATCC TCGAGATCTA CCTAAAAAAA AAAAATTAAC TTCCCAAATG TGGGAGTCTA	120
CTCTGTTCCC TCCTNGTNTT TATTNCTGTN TACTTTYCTA ANATGGTTAA AATGTGTAAN	180
CAATATGTGT CCTTTNACTN KGGKGTGAAC ATTTTTYCTA TTATAAATYC TWAGAAAATA	240
TTNCTATGGN TATGAGATAT TKGATTCCAA GTGCCTKGTA ATTTACTYCT CAAATGTCCC	300
TGATGTKGGA NATTKGTTNC TAGTGTTYCA CTATTTAAAA AACAGNAAT ATCTGTCTNT	360
ATGCTNAGAG CTTNTYAGT TTYCAAATTA TTNCCTTAGG GTAAAATCCT AGAAGTAGAA	420
TTTTTGGGGC AAATTATCTA CATATTTATA ATTGTCTTGG TATTCCAAAT CTCGTTTTCC	480
AAAAGCTTAT ATCAATTTGT ACTTAACACC AG	512

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATTTAAGATG ACTGGGGGTC TCTNCCTAAT CCCATACTCC ACTGGAGAGG ANAAGTGGGA	60
AAGGTTGGTC TAGTTARGGT NGNTGGGGAC CCTCCCAAGA GCTGNAGAAG CAGAGATAAG	120
NAGAGCCTNC TNCTAAATCC ACATGGNCCT YCCAAGGNTC TCATCCTCTA GGACCTACCA	180
CTNCTCAGTC TACTTACTTG TCTYCTGANA TGCTTTCTNG AGGGGNAGAA AACAAAGGAA	240
GAGTAATAAC AAGCAGNAGA AACTGCAGAG AATGNAAAAT AAGTCCATAG GAGAATGTTG	300
NAAATAGAAT CATCCNCCTT TACATATTGT CACTCCAGGA AACTGCCAA GAACCACTCA	360

TTCCTCTAGA TACAMTTCCT GTAGGATCCY CCCAGACTTC CTCCTTAAG CACGTCAGTA 420  
 TTCTCCTTAT TCTCCCTTCA TTTCAACCCT 450

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 766 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGATCTGC CCCAGCCCAC ATTTCTTTTG TTGAATGAGT AGAGAAGACT GAGAAGTATC 60  
 ACTCACCCGT GATGTGGTTT GTCCCTTTTC CAGCCAGTGT GTTGGAATA AAAGTCACCT 120  
 TTCAGAGCTT TGGTCCCCGT AATGCCCGTC TTTCTGTGT CCAGGAATAA CCTTTGNTAC 180  
 TAGGCAGTCC TCTGAAAGAT TTGTAGAAGG TTAAAGTGA AAGGGACTTG GAAGCTCATA 240  
 GAATCCATGC CTCTTCTTTT AGCATCAAGG AATTAGAAGT CCTGAGAGAT GAAGAATGTT 300  
 GTCTTCCCAA CTCAAACCCA TTTCTTGAAG CCATTTCCCT GGTACTGNA TTGGCCACAA 360  
 CCCTTCCCCC TTGNTATCCT CATCCTGCTA ATGCTGTTTT TAATGGCCTG CCAGTCTGGA 420  
 TTTGTCTTTG GCAACCAAAC AATTTTGCTT CACAAGATTC CTACTTAAGG GAAGAGAGGG 480  
 GCTCCTCATT TNTCACTTGT ACAAGAGCAG GGCTGGTCAG CTTTACACAG GTGTCAGATG 540  
 AACCGTCACA ANCCAGANTT NCATGTTGGC CTCAGGAGGG CTTCNAGGTC CAACATCTCG 600  
 ACGTAAGGAG CGTTCACAGT TCTTTCATGC TCAGATAACA GTNCTAACTN CAGCTGTTTC 660  
 ATCCCNAAATC CCTANTTGAG GTCTTAACAT CTATTCCATT TTKCCNACMA GGGTTATNCT 720  
 GTTAACCCTC TNCACCAGAN TTAGANCTGA CTGATNCACT TCCTAG 766

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 327 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATACTTGT ATAGTTCKNT AAGATAATCA CTCTCTCACT CAGACATNNG GNGRARNGCC 60  
 CNTCGATCAC TTGGGANAGG NGAATTGCMA TGTTTAATGA TTGTCANCCM NANAANTAAG 120  
 CTNACAGGGC AAAAACAGCC TYANGTCAGT TCTNTCTCCC TAATCCTCTA GRAKNAAATC 180  
 NNAWRNTRNN ACTCTGNNTC TGTGCCATNA NANATNTTNC ANTTGTATTT ATGNACTCCA 240

CATNGAGTAC ACCTCACTAA WTNTNCTNCT GGGNAACNCC CSCMCCANTT TTTNNTTGNT	300
GANANACARC AATGCTGGCA TACNGTG	327

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 431 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCAGACTTTC ATAACNGTG TTATTATGAA GATTAGAGTN CTGAAGCTTA CTGGATTAGA	60
AGAGNACGAG GGGGTAGCTG CCCCAATATA TTCTAATTTT TCTKGAGGAC CACCAAATNG	120
GMAGAGTGTC TCTGATAGGG AAAAGGAAGA GTTGGAAGGN ATCTTAGCCT CTAGGANAAA	180
AGAACCATTT TTATTGGCCA CCAAAGTTAC ATCTAGTKGC CTACAAATTT ATNTCCAAAC	240
TCCTTATCCT GCCAATTCAG GGTCCTGNAA ACTGATGCCA AACTATAGTT TAGTCTNCTA	300
TCACATGACT GCATTATACA TACCCAATTA TCTGGGMAAA CAGACCTGAT CCAAACACAG	360
TTKGGTNCTT TCCTTNCCTT NCCTTKGTTT AGCCTGTYCC GTCTACTNGG GGTGTCTTKG	420
ATTTGCTCCA G	431

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTTTTTCCA CCAGACTTAC CAAATTTTAG ATGNATGGAA GAACTGTAAA TNCCCATAAA	60
GNTAATCTAT NCATNGACCC CCACCATTAT GATAGAGATC ATNTGGTGAN TAATGAAAGA	120
TGAAACTCTC AGCTGGGAAA GTAANAAGGA ATAGGATGTA AGTATGAGCT CCTGTTTTTT	180
ATTATNTTTA TGGATGCCCC CTCAGAAAAA TATGNAANGG GGTAAGTAC TNGGAAATGG	240
GTNTTTTATG NATAGTAAGT CCCACTCACG AGGTTT	276

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 270 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGAGATCTA AAGCAGATGN AGACTTTNCA CNAATAAAT TTACTGCTTT TTTYCTGTGA	60
NATAAGTTNC GAGAAGGAAA GCTTTKGATT NCTRNATGAG TYCAGTGGAT TATYCTNAGN	120
ACTAGAGTKG NKGTGGAAGN CATGGNACAT TTATATAGWT YWTTTCAGTTC TACACTAAAT	180
GATGGAAGAA TGAGAAATCC TATATGACAA ATAGAAAAGT YCATYCTYCA TAATTGAGAA	240
CATTGAGCAG TTGGATTACC AAGATCTCGA	270

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTAGTTTTA GACTAGTTTC ATTATACTAC CAGTTTCTAA TATGTTGGTT TTTTATTCAC	60
TATTTGATAT ATTTGTTTTA ATATATGTTT TTGTTTTAGC AGGTAAAAGA ATCATAACAA	120
ATGTTTTTAA AAGAACATTA TTATTCTTTA ATAAGTGTCT TTTTATGCAT TTGGCATGCC	180
AACTTTTTTC ATTAACATCT TGGGTATTTT ATAAAAAGAG GGAAAGCTCA ATGTTTAACA	240
GGTAGCTTTT CTTAGGAGCT AAATTAAATA TTTAACAAAT CTCCTTCCCT TCNCCCTTCC	300
CCATCCCTCA AAGNATGGGT GNANTTATCT TTAAGTTTGT GGCTNGCATC CNTGNAAGCT	360
TATGGNTANT CATAGTCTNA CMAAACTAGG GTCACCNAAC TTGGCAGCAG AAATAATCTA	420
GTCTTACTGT GATAACTACC CAATTACTTT ATTATTTTTC CAGTTNCAGT TCCAAATGTT	480
TTGTGGNAAN AATTTTTNCT GTTTGTGATT TTCCAAGCTT AGAGGGGGAA ACCAACTTTC	540
CAGTGTGGA GAGCACTGNA TAGTTTATGN ATTGTGTAAA	580

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTTTCTTAA NACAGAAAAA AATTTACTGA TNGGACATTG TTCTAAGTGT ATTATTGTAT	60
TAAATGGATC ATTTAATTTA ATCTTCATAA CTGACATAGG AGTTGAGTAA CTTGTGTGGT	120
CAAATAGCTA GTAAGTGATG AGTAGGCTGG GCGCAGTGGC TCAAGCCTGT AATCCCAGCA	180
CTCTGGGAGG CTGAGGCAGG CAGATCACTT GAGGTCAGGA GTTTGAGACC AGCCTGGNCA	240
ACATGGNAAA ACCTCGTCTC TACTAAAAAT ACAAAAATTA GCTGGGCGTG GTGGGNGCGC	300
ACTTGTAGNC CCAGNTACTC GGAAGGCTGA GGCAGGAGGA ATCGCTT	347

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 430 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCTCATCATG CTTACGGGG GAGGCTGTGC GGGAAGAATG CTCCCACACA GNATAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCCCG CACAGCATAG AGAAGCCCC GCACAGCATA	120
GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGN ATAGAGAATG CTCTTCACCT	180
CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGGCAA CACATCATTT AAGATAGAAA	240
TTTCTGTATC TTTTAATTC TTTCAAAGTA GTTTTACTTA TTTNCAGATT CTATTTCTTT	300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACAAACAAAA	360
GCTAGGTTTT NTNCATAGGT CTNCTTCNN ATTGAATGAA CGTCTNTCCT CAAATTTANC	420
CCCCCAGGGA	430

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CAAACCCTAT GNGAAATGGA AAGGAACTA TTCTAAAGCA TAAAAGGTAG AAATATATAT	60
ACCACCCATC AAGAAAGATT ATTTTTGNTG AACTCAAGTC ACCAGAGTGG CTAAAGCCCCA	120
GTAGAATGGA AATGATTATA TGGAAGGTGA GGCCAACGGG ACCAGAACAT ACTGTGATAG	180
ACAGNAAGGA GCTGTCTATC TTCTATTCTC CCACAGAAGG AGGTGACTAA GTCANCTGCC	240
CAAGCAATGT TATATCTGCA ATTGATGTNC AGCAGTACAA GTCTGAACAA CTTGGATTGG	300

NTGATTAATG TCCACANTAA ACATACAAGT CNTAATAGCT ATCTCTATAT AGTCTTTGGG 360  
TNTTTACAAG GCACTGNCAC ATNATCTCAC CTATTCCTCC 400

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGNATCCAGA ATTGAGTGNA GNGTTCTCTG GNCCACAGTC TCGGTATCTN CTGTGAAATG 60  
GGGTATAGAT TCTACAATAA AACAAACACA NNGGCCCTAG GTCAGTGTTA ATGGAGATCA 120  
CCANCCACAT TACCACCTCC AACACAGAAT TTTCTTTTTC TTAATNCAAT NCGTNTCTTA 180  
TAAGTCACTT TNCCCCAACT CACCAATCTA GNTAAGAATT TTTACCCTGA GAAAAACAGC 240  
TACACTCTAA AATTGCTNCA AAGAAAATGT CTAACATNTG GAAAGAAGGA CTTAACATGT 300  
GANGNAGACA CTGGCTCCAT CTAGNGGGTG CTTTNTTTTG AAATAATTAT AATNCCNCAT 360  
CAAATTTTNG GGGGNTACAG CTTATTAGGA ACTTGTTATA GAACCAGATT CTGCCACAGA 420  
ANCCACGTGG GTTGACAAGT GGTGNCAGA AGAAAGGTAA TATGGCTTAT NATTAGGGNC 480  
TCNCATCTGC AGAGTAATTG 500

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 460 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAATGCTTG ANNCAAATGT CATCTAGTTC CATCTCTACG ACTCTCATGG GGTCCAAAGA 60  
AGAGTTTTAN TTGAGTTTTA GAATGTGAAG TTGTGAAGTG TCTGAAAAAC TACATGGTGN 120  
TCTGAAAGNC AAACCTTTTAG CCTTGGGGGA GAGCATCTAA GACAGNAGGT GAAGGGNAGG 180  
GGTTAGAACT AGAGGGATTG AAGAATATTA TCCATATAGG TTAGGGTTAG GTNNGGCAAC 240  
GTTTTATAGA ACAAACATTG GCAAGCTACA GCCACAGGCC AGATCTGTCT NCTACCTTCC 300  
CACAAAGGTG TAATAACAAA GTTATTCACA AATGTGTGAA TAACTNNCA TTGGAAAGTG 360  
CCCACGCTCC TNGGTTTATA CATTGTCTGT GGCTGCTTTC AACTACAGT AGCACAGGTG 420  
AGTGTNTGCA CTGGAGACCA TATGCCCCAT AGAGCTTTAA 460

(2) INFORMATION FOR SEQ ID NO:49:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 370 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCAAGCAAC AGTGTGTTAT GCCTATACTC CATGTTTATA TGTGTGTATT AAAAAATGTA	60
TTTGTATATA TGTGTATGTA TAAGTGTGTG TGTGTGTATG ATGATTCTNC TCCCGNTTTG	120
AAGGTGAAAG AAAGCACACC TTTATTTAAG CATAAACTTT GGGTTTCAGA TACTGTCTGG	180
AAAAATGATT TATCTCCAC TTTGAAATTC CAAAATACGT ACATATATTT TTTTTTCTT	240
TTCTTTTTTA GTTTNAGGGT CTTGCTGTGT TGCCCAGGCT GGAGTGCAGT AGTGTGATCA	300
TAGNTCACAC AGNCTCTAAC TCCCAGGNTC AAGNTATCTT CCTGCCCCAG NCTCCTGAGT	360
AGNTGGGACT	370

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAAAAATCA AAGGGAAGNT GGAACCCCTG CCCACCTCTC CATTCCCCAT TCTGCTGGTG	60
GTGNCTGCTC TTCCTCACAG TACCTCCTGA AAAGTTCAGA ATTCAGTTAA TACAGAATTA	120
TTGGGTTGAT TTTCAACGTG TAGTTTAAGA TGAAGAGTTC CGNTTGTTTT AAACCACTTC	180
ACCTAACCTC TTGGTAACGG TAGTCCTGAG AGTTCGCAGT GTCANTGAAA ATCGTCCTGT	240
GACCACGCGT CAAGCTGCTG ATGGGGGACA GAAACTTCCG GGNCATCAT ATCTCCTTGA	300
NCTCGGCCCT CAAATCTGGT AGTTTCTGCA CCGAGGGACA CAGTCCACTG CGATGAAGTA	360
TGTTCAAAAT CGNTTCTTTT AGGGAAGTCC TTCCAAAGTC CAATAGTGNA AGGTGGTCAA	420
GGAAGGATTT GGAAGGAAGN TGNAAAAGTC AGNCGGGAAT CTTGATTTGG NTAGNTGTGG	480
ANANAGGAAA TCACTTGGCC	500

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAGAGGT CTCCTAACAC CCAGACAGTG TAAAAATCCA GTTTTTCTTC CTTTTGGNNG	60
GAGACAGAGT CTCGCACTGT AGCTCAGGCT GGAGTGCAGT GGCAC	105

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGTCCCAGCT ACTCAGGAGG CTGGGGCAGG AAGATAGCTT GAGCCTGGGA GTTAGAGGCT	60
GTGTGAGCTA TGATCACACT ACTGCACTCC AGCCTGGGCA ACACAGCAAG ACCCTAAAAAC	120
TAAAAAAGAA AAGAAAAAAA AAATATATGT ACGTATTTTG GAATTTCAAA GTGGGAGATA	180
AATCATTTTT CCAGACAGTA TCTGAAACCC AAAGTTTATG CTTAAATAAA GGTGTGCTTT	240
CTTTCACCTT CAAAGCGGGA GAAGAATCAT CATAACACAC CACACACTTA TACATACACA	300
TATATACAAA ATACATTTTT TAATACACAC ATATAAACAT GGAGTATAGG CATAACACAC	360
TGTTGCTTGA TAAATATAG GGATCC	386

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATATTTNAT CAAGCAACAG TGTGTTATGC CTATACTCCA TGTTTATATG TGTGTATTAA	60
AAAATGTATT TGTATATATG TGTATGTATA AGTGTGTGTG TGTGTATGAT GATTCTCCTC	120
CCGNTTGAAG GTGAAAGAAA GCACACCTTT ATTTAAGCAT AAACCTTGGG TTTCAGATAC	180
TGTCTGAAAA AATGATTTAT CTCCCCTTT GAAATTCCAA AATACGTACA TATATTTTTT	240
TTTTCTTTTC TTTTTTAGTT TNAGGGTCTT GCTGTGTTGC CCAGGCTGGA GTGCAGTAGT	300
GTGATCATAG NTCACACAGG CTCTAACTCC CAGGNTCAAG CTATCTTCCT GCCCCAGNCT	360
CCTGAGTAGG TGGGACT	377

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 521 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGCAGTAAG CCACGTTTCAT GCCACTGTAC TCTAGCGTGG ATGACAGAGA GAGATCCTGT	60
CTTTGGAAGA AAAAAACAAA AAGAAAAAAA AAAGAGTATG GCCATGGCCT TATAATATAG	120
AAGGGGTCAC ATATTAATCT CTGAAAATGG ATCTCTTGTG GGCTTTCATA CAAGGCAACA	180
GCCACAGAGT ACGTACCTGA AAGCTGCCTG GGNTTAATGG CTGGNAGTAT GTTCTAACTN	240
GTTCAGGNAC CCATGTCACN ACTGGTGGTT ACAGAATGTG AATCTCACAC TGTCCNAAAT	300
CGGTTTTTATT TTAAAANGA ATAATTCTAN TACATTACCT TATAAAAAGT AGGTAACCTA	360
ATTTTGGNTT TAAAAGTGA ATTGAGGGCA GATGCAAGTG GNTCACACCT ATTAATCCCA	420
AATACCTTGG AGAGGGCAAG GTAGGAGGAT TGGTTGGAGC CCAGGAGTCC AAAGACCAGG	480
CTAGGGAATA TTGNAAGAN GTCCTCTCTA CAANAAANAA T	521

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTGCANGAAG CTTTTNTTNC TTTTNGGNGG AGACAGAGTC TTGCTGTGTC ANCCCAGGCT	60
GGGGTGCAGT GGNACAGTCA TAGCTCACTG CAACCTTGAA CTCCCTGGNT CATGCGATCC	120
TCCCACTTCA GCCTCTCAAG TAGCTAGAAC TACAGGTGTG CACCACCATG CCTGACTAAC	180
TTGTTTATTN GNGGGAGAGA GAACGNTCTT GCTATATTGC CTAGGCTGGT CNTTGAACTC	240
TTGGGNTNCA AGCAATCCTC CTACCTTGGC CTCTNCAAGG TANTTGGGAT TNATAGGTGT	300
GAGCCACNTG CATCTGGCCT CAATTCACCT TAAAAATNCA AAATTAGGTT ACCTACTTTT	360
TATAAGGTAA TGTATTAGAA TTATTCTTNN NAAAAATAAA ACCGATTTGG GAAAGNGTGA	420
GANTCACATT CTGTAACCAC CAGTGGTGAA ATGGGTCCCC GAACAAGGTA GAACATACTC	480
CCAGCCATTA ACCCCAGGGA GNGTTCAAGT CCGTNC	516

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 505 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGATCCTGTT TCTTAAACA GAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
TTGTATTAAA TGGATCATTT AATTTAATCT TCATAACTGA CATAGGAGTT GAGTAACTTG	120
TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGGCGC AGTGGNTCAA GCCTGTAATC	180
CCAGCACTCT GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TCAGGAGTTT GAGACCAGCC	240
TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GGCGTGGTGG	300
GTGCGCACTT GTAGTCCCAG CTA CTCTCGGAA GGGTTGAGGC AGGAGGAATC GCTTGGTCCC	360
CGGGAGGGAG AGGTTGNTNG TGNAGCTGAG ATCACGCCAC TNGCACTCCA GGCTGGGNAA	420
CAAAAGGGAG ACCTTTNCTC AAAAAAAAT NAAAATAAAA AGTGATGAGT AGGATTGGGA	480
CCCNAGACAT CTTTCTCCA AGACC	505

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 500 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGCAGNCTC AAACCCTTGT CCTGGGATCA AACAATCCTC CCACCTCAGC CTTCAAAGTA	60
GATAGAACTA CAGGCATGCA CTACCATGCC TAATTTTTTA AAAAAAATT TTTTTTCAGA	120
GATGAGATCT CACTGTGTTT CCCAGGNTTG TCCGGAATC CTGGACTCAA GCGATCCTCC	180
CACCTTGGGC TGCCAAAGTG TTGGGATTAC AGGCATGAGC CACCATGCCT GGCCATACAC	240
TTTTTTTTTT TTTTAAANCA AGACGGAGTC TNGTTCTGTC GCCCAGACTG GAGTGCAGGG	300
GCGTNNATCT TGGCTCACTT GAAAGCTTCG CCTCCCAGGG TTCATGCCGT TCTCCTGNCT	360
CAGCCTCCCA AGTNGGTGGG ACTACAGGNA TCTGCACCAC GNCCGGTTAT TTNTTGGGTT	420
TGNNGNAGGG ACGGGGTTT ACCATGTTAG GCAGGATGAC TTCGGACTTC CNGACCCAAG	480
ATCACCTGCT TCGGCTCCCA	500

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 440 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCCAGA	CGAGCCTGGG	CAACACAGTG	AGACTCTATC	ACTACAAAAA	AATTTTAAAA	60
TTAGCTAAAG	TTGATGGNAC	ATGCCTGCAG	TCCCAGCTAC	TCAGGAGGCT	GGGGCAGGAA	120
GATAGCTTGA	GCCTGGGAGT	TAGAGGCTGT	GTGAGCTATG	ATCACACTAC	TGCACTCCAG	180
CCTGGGCAAC	ACAGCAAGAC	CCTAAACTA	AAAAAGAAAA	GAAAAAAAAA	ATATATGTAC	240
GTNTTTGGGG	AATTTCAAAG	TGGGAGATAA	ATCATTTTTC	CAGACAGTNT	CTTGAAACCC	300
AAAGTTTATG	CTTAAATAAA	GGTGTGCTTT	CTTTCACCTT	CAAANGCGGG	AGAAGGATCA	360
TCATNCACAC	ACACACACTN	ATCATNCACA	TTTTTACAAA	TNCAATTNNN	NAATACAACA	420
CATTTTAACA	TGGGGTTTTG					440

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCTGTT	TCTTAAACA	GAAAAAATT	TACTGATAGN	ACATTGTTCT	AAGTGATTA	60
TTGTATTAAA	TGGATCATTT	AATTTAATCT	TCATAACTGA	CATAGGAGTT	GAGTAACTTG	120
TGTGGTCAAA	TAGCTAGTAA	GTGATGAGTA	GGCTGGGCGC	AGTGGCTCAA	GCCTGTAATC	180
CCAGCACTCT	GGGAGGCTGA	GGCAGGCAGA	TCACTTGAGG	TCAGGAGTTT	GAGACCAGCC	240
TGGCCAACAT	GGNAAAACCT	CGTCTCTACT	AAAAATACAA	AAATTAGCTG	GGCGTGGTGG	300
NTGCGCACTT	GTAGTCCCAG	CTACTCGGAA	GGCTNGAGGC	AGGAGGAATC	GCTTGATCCC	360
NGGGAGGGAG	AGGTTGGTNG	TGANGCTGAG	ATCACGNCAC	TTGNACTCCA	GNCTGGGNAA	420
CAAANGNGAG	ATCTTNTCTC	AAAAAAAAT	AAAANTAAAA	NGTGATGAGT	AGGATTTGGA	480
CCCCAGACAT	CCTNTCTCCA	GGACCTGGNA	TTC			513

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCCTGG NCTCAAGTGA TCCTCTCACC TCAGCCTCCC AAATTGCTGG GATTAGAGTG	60
TGAGCCACTG TGCCTAGCCT GCATATATCT ATTTTAAATG ACTGCTAAAT CTCATTGTAT	120
GAAAATTTAT GTCCTAGCTA TAAAATTTGN TAGCACATGT TTAATTTTTT CTAATTTTCTAG	180
ATGTTTTTAAA CTAATATTTT CCAAAGTATA GTATGGCATT TTAGGTATGA TATGATCTTT	240
NNTCCTCTTC GTACTCATTT TTATAGTTAT GGCCTGTGCA ACTGGTTTCC CATTTATATG	300
AATGATACAG AGCTTCCTAT TAAGAAAAAG TTCAGCTTGG GGAAAAAAA AGTGAATTGT	360
CAACTTNGAG GGAAAAAAGT GAATTATTGG	390

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTTCA GTATATGGTA	60
AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC ACTGGAGTGT TTTCTTTTCT	120
CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC ATCCCATAAC TCTTCAGTAA	180
ATCATTAATT AGCTATAGTA ACTTTTTTCAT TTGAAGATTT CGGCTGGGCA TGGTAGCTCA	240
TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG ATCACCTAAG CCCAGAGTTC	300
AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA GAAAATACAA AAATTNGNCG	360
GGNATG	366

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AACACCAGGG NCATGAGGGC ACTAATCATA ATGAGATATG CCTGCTGGAG TCGAAGTGGA	60
CCTTTCCAGT GAATGGAAAT CATTCCCACC ACACCAAAAT TCCAGATCAG GAGTGNAACA	120
GTAATGTAGT CCACAGCAAC GTTATAGGTT TTAAACACTT CCCTGAAAAA AAATTACACA	180
GATTTTAAAA GATGTACAAT AATTTCCACC AAAACATTAT TTAGAATAAT GTGATGGCTC	240
CCAAACATTA GATATTAATN TCCCACCTTT ATAATTTTAC CATAACCTAT ATCAACTGTG	300

CTATTATTTA TTTAATNCTT CCCTNTAAAT TAATTTACTC TTTTTTTGTT TTTGTTTTTG	360
NGTTTGGAGC CAGTGTCTCA TTTTGGTTGC CCAGGCTTGG AGTAAAGTGG GTGCAATCAC	420
GGCTCAACTG NAGTCTTTNC CTCNNGGAGA TCAGGTNGGT CTTCCCCAGG TCCAANCTCC	480
TAAGTTGGTT NGGANAAC	498

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 469 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAAACAACAG GGNCATGAGG GCACTAATCA TAATGAGATA TGCCTGCTGG AGTCGAAGTG	60
GACCTTTCCA GTGAATGGAA ATCATTCCCA CCACACCAA ATTCCAGATC AGGAGTGAAA	120
CAGTAATGTA GTCCACAGCA ACGTTATAGG TTTTAAACAC TTCCCTGAAA AAAAATTACA	180
CAGATTTTAA AAGATGTACA ATAATTTCCA CAAAACATT ATTTAGAATA ATGTGATGGC	240
TCCCAAACAT TAGATATTAA TNTCCACCT TTATAATTTT ACCATAACCT ATATCAACTG	300
TGCTATTATT TATTTAATNC TTCCCTCTAA ATTAATTTAC TCTTTTTTTG TTTTTGTTTT	360
TGTGTTTGA GCCAGTGTCT CATTTTGGTT GCCCAGGCTT GGAGTAAAGT GGGTGCAATC	420
ACGGCTCAAC TGNAGTCTTT ACCTCCCGGA GATCANGTTG GTCTTTCCC	469

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 370 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTTATCAAG TACCTCCCTG AATGGACTGN GTGGCTCATC TTGGCTGTGA TTTCAGTATA	60
TGGTAAAACC CAAGACTGAT AATTTGTTTG TCACAGGAAT GCCCCTGAGT AGTGTCTTCT	120
TTCCTCATCT CTTTATCTTG ATTTAGAGAA AATGGTAACG TGTACATCCC ATAACCTTC	180
AGTAAATCAT TAATTAGCTA TAGTAACTTT TTCATTTGAA GATTTCGGCT GGGCATGGTA	240
GCTCATGCCT GTAATCTTAG CACTTTGGGA GGCTGAGGCG GGCAGATCAC CTAAGCCCAG	300
AGTTCAAGAC CAGCCTGGGC AACATGGCAA AACCTCGTAT CTACAGAAAA TACAAAAATT	360

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 316 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
GTCATGGTGT TGGCGGGGAG TGTCTTTTAG CATGCTAATG TATTATAATT AGCGTATAGT      60
GAGCAGTGAG GATAACCAGA GGTCACCTCTC CTCACCATCT TGGTTTTGGT GGGTTTTGGC      120
CAGCTTCTTT ATTGCAACCA GTTTTATCAG CAAGATCTTT ATGAGCTGTA TCTTGTGCTG      180
ACTTCCTATC TCATCCCGNA ACTAAGAGTA CCTAACCTCC TGNAAATTGA AGNCCAGNAG      240
GTCTTGGCCT TATTTNACCC AGCCCCTATT CAAAATAGAG TNGTTCTTGG NCCAAACGCC      300
CCTGACACAA GGATTT                                     316
```

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 448 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
CTGCAGNCCG GGGGATCCTG GTAAAAGTCA CAAGGTCAGC CTAATAAGC AGGGAAAACT      60
AAAGGCAAGT AAACACGTGC AGACAAAAAA AGGGATAAAG AAAAGGAATT AAGAACTAG      120
CATTTTTTAAN GTGGGGGAGG TGAATGCTTC CCAGAATGGG TTTATATCAC TTGCTTGNGG      180
GCCTTCTGAG TGTGGNAAC AACCTGTCAT CATCACACAT ACCTGTCATC TTTAATGGTC      240
TCCATACATT ACTAATAGAT TATACAGATG GCCATCACTT AACACTTCCA CTCACTCAAT      300
TTGTNCAACA TGCAAGGTTA CCCTCTTTTT TNGCTTACNG CCACAAAGCA TTGGANAAGG      360
TTTGTGATTT TTACTAGCCN CCACTTCATC AAATTTAAGC ATTTTCTTTT TCCTNTTAAC      420
ANCCAGGACA GGNTTNAACN AAGGAAAT                                     448
```

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 450 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGCAGCTCC AAGCACCTTT TTCAAATTCA GCTTCTGTG ATTTTCAGACC ACATATGCAA	60
GGAACCTATCT TACCTTAATT AATAAGACTT TAAAATCCTT GTGTCAGAGG CGTTTGGACC	120
AGAGCAACTC TATCTTGAAT AGGGGCTGGG TAAAATAAGG CCAAGACCTA CTGGGCTGCA	180
TTTGCAGGAG GTTAGGTACT CTTAGTTACG GGATGAGATA GGAAGTCAGC ACAAGATACA	240
GCTCATAAAG GATCTTGCTG ATAAACTGG TTGCAATAAA GAAGCTGGNC AAAACCCACC	300
AAAACCAAGA TGGTGAGGAG AGTGACCTCT GGTATCCTC ACTGNTCACT ATACGNTAAT	360
TATTATACAT TAGCATGCTA AAAGACACTC CCCGCAACAA CCATGANAGG TTTACAAGTT	420
NCCATGGNAA CGNNCCCGGA NGNTANCTTG	450

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGNAGCCTC CACCACCCAG GTTCAGGTGA TTCTCCTGCC GTAGNCTCAT GAGTAGNTGG	60
GATTACAGGC ATGTGCCACC ATGCCCGACT AATTTTTATA TTTTGTAGTAG AGACGGGGTT	120
TCACCATGTT GGGCAGGCTG GTCTCAAACCT CCTGACCTCA AGTGATCTGC CCACCTTGGC	180
CTCCCAAAGT GCTGGGATTT CAGGCGCCTG GCCTGTTACT TGATTATATG CTAAACAAGG	240
GGTGGATTAT TCATGAGTTT TCTGGGAAAG AGGTGGGCAA TTCCCGGAAC TGAGGGATCC	300
CTCCCCTTNN NAGACCATAC AAGGTAACCT CCGGACGTTG GCATGGNATC TTGTTAAACT	360
TGTCATGGNG TTGGGGGGGA GTGTCTTT	388

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGCAGAAAGT ATGTTTCCTG TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA	60
ACACATAAAT TCTTTTCCAC CTCAGGNCA TTGGGCGCCC ATTGCTCTTC TGCCTAGAAT	120

ATTCTTTCCT TTTCTAACTT TGGTGGATTA AATTCCTGTC ATCCCCCTCC TCTTGGTGT	180
ATATATAAAG TNTTGGTGCC GCAAAAGAAG TAGCACTCGA ATATAAAATT TTCCTTTTAA	240
TTCTCAGCAA GGNAAGTTAC TTCTATATAG AAGGGTGCAC CCNTACAGAT GGAACAATGG	300
CAAGCGCACA TTTGGGACAA GGGAGGGGAA AGGGTTCTTA TCCCTGACAC ACGTGGTCCC	360
NGCTGNTGTG TNCTNCCCCC ACTGANTAGG GTTAGACTGG ACAGGCTTAA ACTAATTCCA	420
ATTGGNTAAT TTAAAGAGAA TNATGGGGTG AATGCTTTGG GAGGAGTCAA GGAAGAGNAG	480
GTAGNAGGTA ACTTGAATGA	500

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTGCAGAGTA ATTGCAACTG GAGTTGTCTT AAGATAATGT CACATATCCA TCTTCCCCTT	60
GTTTCTCATT CACAGAAAAA CATTTTTTATT CCAGGTGCCA ATATTCCCAG CCAAAAAGAC	120
TTTACTTCTG ACTCCCTTAT ATTTAGGATG GCTATGAGAA CAAGTAAGGG CAATGACTTC	180
TAGGGAGATG TGTGTGTAT GGAAGTTCTA AGGAGAGAAT TCTGCTGACA TGTCCTATGT	240
TCTTTTCTCC CCTACTCCTT CCTACTGTCA GAAATGAAGG CTAGGGCTCC AGCCTGGACC	300
CTGAAGTAAG CTAGAGGTTA GAAGCTAAAG AAGAAAGAAG GAGATTGAGT CCTTGGATGA	360
ACGTGAAGCC ACCCTACTAA TCTGGACTGN CTACCTCTGN ACTACTCTAT GAGAGAGAAA	420
GTATGTGCAT TATTT	435

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATGCTCTTT GTCCCTGTGA CTCTCTGCAT GGTGGTGGTC GTGGNTACCA TTAAGTCAGT	60
CAGCTTTTAT ACCCGGAAGG ATGGGCAGCT GTACGTATGA GTTTGGTTTT ATTATTCTCA	120
AAGCCAGTGT GGCTTTTCTT TACAGCATGT CATCATCACC TTGAAGGCCT CTGCATTGAA	180
GGGGCATGAC TTAGCTGGAG AGCCCATCCT CTGTGATGGT CAGGAGCAGT TGAGAGAGCG	240

AGGGGTTATT ACTTCATGTT TTAAGTGGAG AAAAGGAACA CTGCAGAAGT ATGTTTCCTG	300
TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA ACACATAAAT TCTTTTCCAC	360
CTCAGGGGCA TTGGGCGCCC ATTGNTCTTC TGCCTAGAAT ATTCTTTCCT TTNCTNACTT	420
GGNGGATTA AATTCCTGT	439

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCCATCTCTA CGACTCTCAT GGGGTCCAAA GAAGAGTTTT AATTGAGTTT TAGAATGTGN	60
AGTTGTGAAG TGTCTGAAAA ACTACATGGT GNTCTGAAAG NCAAACTTTT AGCCTTGGGG	120
GAGAGCATCT AAGACAGNAG GTGAAGGGGA GGGGTTAGAN CTAGAGGGAT TGAAGAATAT	180
TATCCATATA GGTTAGGGTT AGGTGTGGCA ACGTTTTATA GAACAAACAT TGGNAAGCTA	240
CAGACACAGG CCAGNTCTGT CTNCTACCTN TCCACAAAGG TGTNATAACA AAGTTANNCA	300
CAATGTGTG AATAAACT	318

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTTGG ATATATCAGT	120
AATAGTGCTT TTTCNTTTTT TTTTTTTNTT TTTTTTNNTT TTNGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 489 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGCAGNTGA GCCGTGATTG CANCCACTTT ACTCCNAGCC TGGGCAANCA AAATGAGACA	60
CTGGCTNCAA ACACAAAAAC AAAAACAAAA AAAGAGTAAA TTAATTTAAA GGAAGTATT	120
AAATAAATAA TAGCACAGTT GATATAGGTT ATGGTAAAAAT TATAAAGGTG GGATATTAAT	180
ATCTAATGTT TGGGAGCCAT CACATTATTC TAAATAATGT TTTGGTGGAA ATTATTGTAC	240
ATCTTTTAAA ATCTGTGTAA TTTTTTTTCA GGAAGTGTT TAAAACCTAT AACGTTGCTG	300
TGGACTACAT TACTGTTGCA CTCCTGATCT GGAATTTTGG TGTGGTGGGA ATGATTTCCA	360
TTCACTGGAA AGGTCCACTT CGACTCCAGC AGGCATATCT CATTATGATT AGTGCCCTCA	420
TGGCCCTGGT GTTTATCAAG TACCNCCTG AATGGACTGG GTGGCTCATC TTGGCTGTGA	480
TTTCAGTAT	489

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 449 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGCAGNCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCACC ATGCCCCGGCT AATTTTTGTA TTTTCTGTAG ATACGAGGTT	120
TTGCCATGTT GCCCAGGCTG GTCTTGAAC CTGGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA	240
AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCTGTGA	360
CAAACAAATT ATCAGTCTTG GGTTTTACNA TATACTGAAA TCACAGCCAA GATGAGCCAC	420
GCAGTCCATT CAGGGAGGTA CTTGATAAA	449

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 490 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGCCGT TCCCGACCCG AGCCTGGTGC CCCTTCCCCA TTATGATCCT TNTCGCTTCC	60
GGCGGCATCG GGATGCCCCG CGTTGCAGGC CATNCTGTCC CAGNCAGGTA GATGACGACC	120
ATCAGGGACA GCTTCAAGGA TCGCTCGCGG CTCTTACCAG CCTAACTTCG ATCATTGGAC	180
CGCTGATCGT CACGGCGATT TATCCCGCCT CGGCGAGCAC ATGGAACGGG TTGGCATGGA	240
TTGTAGGCGC CGCCCTATAC CTTGTCTGCC TCCCCGCGT TGCCTCGCGG TGCATGGAGC	300
CGGNCCACCT CGACCTGAAT GGAANCCGGC GGCACCTCGC TAACGGATTC ACCACTCCAA	360
GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC NCAAAACCAAC CCTTGGCAGA	420
ACATATCCAT CGCGTCCGCC ATCTCCANCA GCCGCACGCG GCGCATCTCG GGCAGCGTTG	480
GGTCCTGCAG	490

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 470 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGCAGTGTT TAAAAAATAA AATAAACTAA AAGTTTATTT ATGAGGAGTA CACTGCTTTC	60
TTGTAAACAC ATGTACAAGC CATATAATAG AGTTCATTTT NNACCCTAGT TACGGAAACA	120
CTAGAAAGTC TNCACCCGGC CAAGATAACA CATCTTTAGG TAAAAATAGC AAGAAATATT	180
TTATGGGTTG TTTACTTAAA TCATAGTTTTT CAGGTTGGGC ACAGTGGNTC ATGCCTGTAA	240
TCCCAGCACT TTATGCGGCT GAGGCAGGCA GATCAGTTGA GGTCAGAAGT TTGAGACCAG	300
CCTGGGCAAT GTGGCAAAAC CTCATCTCCA CTAAAAATAC AAAAATTAGC CAGGCATGGT	360
GGTGACACAC TGTTAATTCC CAGCTACTTG GGAGGNTTGA GACAGGAGGG TCGCTTGNC	420
CTAGGAGGGA AGAAGTTGNA GGGANCTTAA TGTCAC TGCA CTCTAGNTTG	470

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 445 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CACTCAATTC TGAATGCTGC CATCATGATC AGTGTCATTG TTGTCATGAC TANNCTCCTG	60
GTGGTTCTGT ATAAATACAG GTGCTATAAG GTGAGCATGA GACACAGATC TTTGNTTTCC	120
ACCCTGTTCT TCTTATGGTT GGGTATTCTT GTCACAGTAA CTTAACTGAT CTAGGAAAGA	180
AAAAATGTTT TGTCTTCTAG AGATAAGTTA ATTTTtagTT TTCTTCCTCC TCACTGTGGA	240
ACATTCAAAA AATACAAAAA GGAAGCCAGG TGCATGTGTA ATGCCAGGCT CAGAGGCTGA	300
GGCAGGAGGA TCGCTTGGGC CCAGGAGTTC ACAAGCAGCT TGGGCAACGT AGCAAGACCC	360
TGCCTCTATT AAAGAAAACA AAAACAAAT ATTGGAAGTA TTTTATATGC ATGGAATCTA	420
TATGTCATGA AAAAATTAGT GTAAA	445

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 496 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CCTGTATTTA TACTGAACCA CCAGGAGGAT AGTCATGACT ACAATGACNC TGATCATGAT	60
GGCAGCATTC AGAATTGAGT GCAGGGCTCT CTGGCCCACA GTCTCGGTAT CTTCTGTGAA	120
TGGGGTATAG ATTCTACAAT AAAACAAACA CAAAAGCCCT AGGTCAGTGT TAATGGAGAT	180
CACCAACCAC ATTACCACCT CCAACACAGA ATTTTCTTTT TCTTAATTCA ATTCGNATCT	240
TATAAGTCAC TTTTCCCCAA CTCACCAATN CTAGCTAAGA ATTTTTAACC TGAGAAAAAC	300
AGCTACACTC TAAAATTGCT TCAAAGAAAA TGTCTAACAT ATGGAAAGAA GGACTTAACA	360
TGTGAAGCAG ACACTGGCTC CATCTAGTGG GTGCTTTATA TTGAAATAAT TATAATACCT	420
CATCAAATTT TTTNGGGTAC AGNTTATTAG GAACTTGGTA TGGAACCAGA TTCTGCCACA	480
GAAACCACGN GGGCTG	496

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 496 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
CATTAGATAA TGGNTCAGGG TGGCCAAGGC TCCGTCTGTC GTTGTGCTCC TGCCGTTCTC      60
TATTGTTCATT CTATAAGCAC AAGAAAAACA TTTTCAGTAA ATCAGATTCT CAGCAGAATC      120
AAGGTAACGG TTAGACCTGG GATTAACAAC AGACCCGTCA CTATGAGTTC TAAAAACCTG      180
AAGCAAGAAA AAACAATGTA CAGGAAGTAT GCAGTTTAAA AGTCTAGATT ATCTATCATT      240
GTTCACTGAA GGCATTCAGG TCCTCTCTTT TACCTGGGTC TTGGNTTGCT CCATTCTCTC      300
TGTTTCATCCC AACATACACA ATTGTACTTA TCCTTTGAGA TGTACCTTAA ATACTGACAC      360
CTGCATGAAA ACTTGTTTAC TGGCTGCAGG TCCAAGCACC TTTTTCNAAA TTCAGCTTTC      420
TGTGATTTCA GACCACATAT GCAAGGAACT ATCTTACCTT AATTAATAAG ANTTTAAAT      480
CCTTGTGTCA GAGGCG                                         496
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
AGGANCGCTT GGGCCCAGGA GTTACAAGC AGCTTGGGCA ACGTAGCAAG ACCCTGCCTC      60
TATTAAAGAA AACAAAAAAC AAATATTGGA AGTATTTTAT ATGCATGGAA TCTATATGTC      120
ATGAAAAAAT TAGTGTAATA TATATATATT ATGATTAGNT ATCAAGATTT AGTGATAATT      180
TATGTTATNN NGGGATTTCA ATGCCTTTTT AGGCCATTGT CTCAAAAAAT AAAAGCAGAA      240
AACAAAAAAA GTTGTAAC TG AAAAATAAAC ATTTCCATAT AATAGCACAA TCTAAGTGGG      300
TTTTTGNTTG TTTGTTTGNT TGTGAAGCA GGGCCTTGCC CTNCCACCCA GGNTGGAGTG      360
AAGTGCAG                                         368
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
GAATTCCTTT TTTTTTTTTT TTTTTTTTTT TTNCTCCTAA TGTTTTTATT GTNCCTTAGA      60
TAACTGGATA GNACAAAGTT NGNCTTNGTT TTTTACTTAA AAAACGTACT TTCCGCATAC      120
```

TGTNGCCCGT ATGACTTTCC TGTCCCATCG GAAACCAGAG TTTCCCCAGG TGAGCCCTTC	180
CTATCTGNNG NTACATGATT TAGCTAATTT AACAGAAGA GAGTAATTCC TTNGGATTAT	240
TATCAACATG AACTTGGAC TATGTCTCTA TAAGGGTGAA CACTGATTTT TTTTTCTTT	300
TTAGAAACAA AAACCATCCA CTTATTAATC CAAACTACGG GATTGGATTT ACAACAATCA	360
TCGCATNAAC TGAACATACG AAGTTACCAC TCAAGGGAAT NACAGAAGAA CGTTGNACAA	420
TNTNTCTTAC GGGGTACGNG AATTCAAACA ATGTGGGGAN AGGAACTTCA NTCTACAAAN	480
TCTGACCATC GNTTCAGTAT	500

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCCTTT ACTCTTCTTT AATTCTACCG TCTTTGGGCA TACATCTCAT TTGNTGTGGA	60
AGAAGGTCTG ACAGNAGGGC TGACAGCACC GATTCATAAC ACATTCTTTT CATCATACAA	120
AGAGTAAGAC CCTAGAATAA TGGGACCATC TGCTACCACG ACAGAGCTGC CTTACTGGCT	180
GTAGAAAAAG ACTGCTTGTG TGGGAGAGAA GAATGAGGAC AGAGGAGGCA TCTGGGGCAA	240
GTGAGCGTAC AAGTATNTCT ACAAATTCAG AATTTGGTGG AAAATCCAAA TTTGNCTTCA	300
ACATGATAGA GAATTGATGA GAAAATAGCT GTNCTGTTTC CAAAATTTAC TGAATTTGGG	360
AACCTGAGGT TAAAACTTTT AGGATNAAGC AACTCAGGTT CAAGACTTNG NCTNGGGAAG	420
GAATGGAAAC ACAGACGGGA ATGAGTNTCA	450

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAACTGTATT TATACAGNAA CCACCAGGAG GATAGTCATG ACAACAATGA CAAACTAGGA	60
ATAGCCCCCT TTCACTTCTG AGTCCCAGAG GTTACCCAAG GCACCCCTCT GACATCCGGC	120
CTGCTTCTTC TCACATGANA AAAACTAGCC CCCAGTNTGA TCCGCAGGTN GAGGAATNCC	180



CCGGGTCGAG GTTCGGATCC TGGATGACAG ACCCTCTCGC CCCTGAAGGN GATAACCGGG 240  
 TGTGGTACAT GGACGGNTAT CACAACAACC GCTTCGNACG TGAGTACAAG TCCATGGTTG 300  
 ACTTCATGAA CACGGACAAT TTCACCTCCC ACCGTCTCCC CCACCCCTGG TCGGGCACGG 360  
 GGNAGGTGGT CTNCAACGGT TCTTTCTNCT TCAACAAGTT CCAGAGCCAC ATCATCATCA 420  
 GGT TTGGACC TGAAGANAGA GAACATCCTC 450  
 (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGATCCCTCC CCTTTT TAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA 60  
 AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA 120  
 TAGTGAGCAG TGAGGATAAC CAGAGGTCAC TCTCCTCACC ATCTTGTTTT TGGTGGGTTT 180  
 TGGCCAGCTT CTTTATTGCA ACCAGTTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT 240  
 GCTGACTTCC TATCTCATCC CGTAACTAAG AGTACCTAAC CTCCTGCAA TNGCAGCCCA 300  
 GTAGGTCTTG GNCTTATTTT ACCCAGCCCC TATTCAAGAT AGAGTTGCTC NTGGTCCAAA 360  
 CGCCTCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGGT CCTTGGATAT 420  
 GTGGTCTGAA ATCACAGAAA GCTGAATTTG GAAAAAGGTG CTTGGAGCTG CAGCCAGTAA 480  
 ACAAGTTTTTC ATGCAGGTGT 500

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGCAGTGAG CCAAATCGT GCCACTGCAC TTCACTCCAG CCTGGGTGAC AGGGCAAGGC 60  
 CCTGCTTCAA CAAACAAACA AACAAACAAA AACCCACTTA GATTGTGCTA TTATATGGAA 120  
 ATGTTTATTT TTCAGTTACA ACTTTTTTTT TTTTCTGCTT TTATTTGTTG AGACAATGGC 180  
 CTAAAAAGGC ATTGAAATNC CAAAATAACA TAAATTATCA CTAAATCTTG ATAATAATC 240  
 ATAATATATA TATTTTACAC TAATTTTTTC ATGACATATA GATTCCATGC ATATAAAATA 300  
 CTTCCAATAT TTGTTTTTTT TTTTCTTTAA TAGAGGCAGG GTCTTGCTAC GTTGCCCAAG 360

CTGCTTGTGA ACTCCTGGGC CCAAGCGATC CTCCTGCCTC AGCCTCTGAG CCTGGCATTA	420
CACATGCACC TGGCTTCCTT TTTGTNTTTT TTGAATGTTT CACAGTGAGG AGGAAGAAAA	480
CTNAAAATTA ACTTATCTCT	500

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGCAGATGA GAGGCACTAA TTATAAGCCA TATTACCTTT CTTCTGACAA CCACTTGTCA	60
GGCCACGTGG TTTCTGTGGC AGAATCTGGT TCTATAACAA GTTCCTAATA AGCTGTAGCC	120
AAAAAAATTT GATGAGGTAT TATAATTATT TCAATATAAA GCACCCACTA GATGGAGCCA	180
GTGTCTGCTT CACATGTAA GTCCTTCTTT CCATATGTTA GACATTTTCT TTGAAGCAAT	240
TTTAGAGTGT AGCTGTTTTT CTCAGGTAA AAATTCCTAG CTAGGATTGG TGAGTTGGGG	300
AAAAGTGACT TATAAGATAC GAATTGAATT AAGAAAAAGA AAATTCCTGTG TTGGAGGTGG	360
TAATGTGGGT GGTGATCTTC ATTAACACTG ANCTAGGGNT TTGGGGTTTG GTTTATTGTA	420
GAATCTATAC CCCATTCANA GAAGATACCG	450

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCAGCCAG TAAACAAGTT TTCATGCAGG TGTCAGTATT TAAGGTACAT CTCAAAGGAT	60
AAGTACAATT GTGTATGTTG GGATGAACAG AGAGAATGGA GCAAGCCAAG ACCCAGGTAA	120
AAGAGAGGAC CTGAATGCCT TCAGTGAACA ATGATAGATA ATCTAGACTT TTAAACTGCA	180
TACTTCCTGT ACATTGTTTT TTCTTGCTTC AGGTTTTT TAG AACTCATAGT GACGGGTCTG	240
TTGTTAATCC CAGGTCTAAC CGTTACCTTG ATTCTGCTGA GAATCTGATT TACTGAAAAT	300
GTTTTTCTTG TGCTTATAGA ATGACAATAG AGAACGGCAG GAGCACAACG ACAGACGGAG	360
CCTTGGCCAC CCTGAGCCAT TATCTAATGG ACGACCCAGG GTAACCTCCG GCAGGTGGTG	420
GAGCAAGATG AGGAAGAAGA TGAGGAGCTG ACATTGAAAT ATGGCGGCNA GCATGTGATC	480

## (2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 499 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

CTGCAGTGTT CCTTTTCTCC ACTTAAACAA TGAAGTAATA ACCCCTCGNT CTCTCAACTG      60
CTCCTGACCA TCACAGAGGA TGGGCTCTCC AGCTAAGTCA TGCCCCTTCA ATGNAGAGGC      120
CTTCAAGGTG ATGATGACAT GCTGTAAAGA AAAGCCACAC TGGGTTTGAG AATAATAAAA      180
CAAAACTCAT ACGTACAGCT GCCCATCCTT CCGGGTATAA AAGCTGACTG ACTTAATGGT      240
AGCCACGACC ACCACCATGC AGAGAGTCAC AGGGACAAAG AGCATGATCA CATGCTTGGC      300
GNCATATTTT AATGTCAGNT CCTCATCTTC TTCCTCATCT TGNTCCACCA CCTGCCGGGA      360
GTTACNTTGG GTCGTCCATT AGATAATGGG TCAGGGTGGC CAAGGCTCCG TCTGTCGTTG      420
TGCTCCTGCC GTTCTCTATT GTCATTCTAT AAGCACAAGA AAAACATTTN CAGTAAATCA      480
GATNCTCAGC AGAATCAAG                                     499

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## (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

TAACTCCCAG GNTCAAGATN TCTNCCTGCG TTAGCCTCCT GAGTAGCTGG GACTATAGGT      60
ATGTGCCACT ATTCCTGAAA ACATAATCAG TTTTGAAGGT AGTGTCTGGG CTGGGCGCAG      120
TGGNTCACGC CTTCAATCCC AGCACTTTGG GAGGNCGAGG TGGGCGGATC ACCTGAGGTC      180
AGGAGTTCGA GACCAGCCTG ACCAACATGG GATAAGACTC CATCTCTACT AAAAATACAA      240
AAAATTAGCC AGGCATGGTG GNGCATGCCT GTAATCCCAG CTACTCAGGA GGNTGAGGNA      300
GGAGAATTGG TTGGAACCTA GGAAGCAGAG GCTGTGGTGG AGCCGAGATC GCACCATTTG      360
ACTCCAGGCT GGGNAACAAG AGTGAAAATC CNTCTTAAAA AAAAAAAAAA AAAGGTAGNG      420
TTTTGNCCGG NGCGGGGGGT CACGCCTGTA ATCCCAGNAT TGGGGANGGC AAGNGGGGGG      480
GTCANNANGN NAGNAGTCCG                                     500

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(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCTGCT GACATGTCCT ATGTTCTTTT CTCCCCTACT CCTTCCTACT GTCAGNAATG	60
AAGGGTAGGG CTCCAGCCTG GACCCTGAAG TAAGCTAGAG GTTAGAAGCT AAAGAAGAAA	120
GAAGGAGATT GAGTCCTTNG ATGAACGTGA AGCCACCGTA CTAATCTGGA CTGCCTACCT	180
CTGCACTACT CTATGAGAGA GAAAGTATGT GCATTATTTA AACCAGTTGG GTTGATTTTC	240
TATTAACAAA GTCAGAAACA TCTCTGTAAA AAGCCAGACT GAATATTTTA AGCTCTATGG	300
GTCATATGGT CTCCAGGGCA AACACTCAAC TGTGCTACTG TAGTGTGAAA GCAGGCACAG	360
ACAATGTATT AACCAAGGAG GGTGGTCACT TTCCAATGAA AGTTTATCAC AAATTGGNGA	420
ATACTTG GTA TTACACNNG GGGGAAGGTA GGAGAAGATC TTGCCTGTGG TTGTNGNTGG	480
CAATGTTGGT CTTTATACG NG	502

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCTCTC CTTAGAAGTT CCATACACAA CACATCTCCC TAGAAGTCAT TGCCCTTACT	60
TGTTCTCATA GCCATCCTAA ATATAAGGGA GTCAGAAGTA AAGTCTGGNT GGCTGGGAAT	120
ATTGGCACCT GGAATAAAAA TGTTTTTCTG TGAATGAGAA ACAAGGGGAA GATGGATATG	180
TGACATTATC TTAAGACAAC TCCAGTTGCA ATTACTCTGC AGATGAGAGG CACTAATTAT	240
AAGCCATATT ACCTTCTTTC TGACAACCAC TTGTCAGCCC ACGTGGTTTC TGTGGCAGAA	300
TCTGGTTCTA TAACAAGTTC CTAATAAGCT GTAGCCAAAA AAATTTGATG AGGTATTATA	360
ATTATTTCAA TATAAAGCAC CCACTAGATG GAGCCAGTGT CTGCTTCACA TGTTAAGTCC	420
TTCTTTCCAT ATGTTAGACA TTTCTTTGAA GCAATTTTAG AGTGTAGCTG TTTCTCAGGT	480
TAAAATTCTT AGTAG	495

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 500 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TATGGTTGCC TATTCTTGTC ACAGTAACTN AACTGATCTA GGAAAGAAAA AATGTTTTTGT	60
CTTCTAGAGA TAAGTTAATT TTTAGTTTTTC TTCCTCCTCA CTGTGGAACA TTCAAAAAAT	120
ACAAAAAGGA AGCCAGGTGC ATGTGTAATG CCAGGCTCAG AGGCTGAGGC AGGAGGATCG	180
CTTGGGCCCCA GGAGTTCACA AGCAGCTTGG GCAACGTAGC AAGACCCTGC CTCTATTAAA	240
GAAAACAAAA AACAAATATT GGAAGTATTT TATATGCATG GAATCTATAT GTCATGAAAA	300
AATTAGTGTA AAATATATAT ATTATGATTA GTTATCAAGA TTTAGTGATA ATTTATGTTA	360
TTTTGGGATT TCAATGCCTT TTTAGGCCAT TGTCTCAAAA AAATAAAAGC AGGAAAACAA	420
AAAAAGTTGT AACTTGAAAA ATAAACATTT CCATATTTAT AGCCAACTAA GTGGGTTTNG	480
GGTNGGTTGG GTTGGTTGGT	500

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 385 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TTATCATTA AAGGTCCCAC AACCTTAAA AAGTACAGAT TTTTTTTTTTC TTNGTGGAGA	60
CAGGGTCTCA CTTGGTCGCC CAGACTGGAG TGCAGTGGCA CGATCTCAGT TCACCACAAC	120
CTCTGCCTCC TGGGTTCAAG CAATNCTCGT GCTTAAGCCT CCTGAGTAGG TGGAACCACG	180
CGTGCGCGCC ACCACGCTAG GTTNATTGTG GCTTTTTTTAG TAGAGACAGG GTTTCGCCAT	240
GTTGCCCAGG CTGGTCTCAN ATTCCNGACC TCAAGTGATC CGNCCGCCTC AGACTCCCAA	300
AGTGNTGAGC ATTACAGNTG TGTACCACTA TGTCCCNGNC CNCATCTCTC TTTAAAACAN	360
CTTNCATTTA CCTAGTCCAC TCCTG	385

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACCTAGAAA AGAAAGCATT TCAANNTAAT TAACAGGTCC CACAACCCTT AAAAAGTACA	60
GATTTTTTTTTT TTCTTTNNGG AGACAGGGTC TCACTTTGTC GCCCAGACTG GAGTGCAGTG	120
GCACGATCTC AGCTCACCAC ANCCTCTGCC TCCTGGGTTC AAGNANTTCT CGTGCTTANG	180
CCTCCTGAGT AGGTGGAACC ACGCGTGTGC GCCACCACGC TAGGCTACTT TNTGTATTTT	240
TAGTAGAGAC AGGGTTTCGC CATNTTGCCC AGGCTGNTCT CAAATTCCTG ACCCNCAAGT	300
GATCCCCCN CCTTCAGTAC TCCCCATCAG	330

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 382 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGTGGNCGTT CTAGAACTAG TGGCNCCCAA GGNAGAAGAA GTTTTCTTAG TACAGAACAA	60
AATGAAANGT CTCCCATGTC TACTTCTTTC TACACAGACA CGGCATCCAT CCGTTTTTCT	120
CANTCTTTCC NCCACCTTTC CCGTCTTTCT ATTCCACAAA GCCGNCATTG TCATCCTGGC	180
CCNTTCTCAA TGAGCTGTTG NNTACACCTC CCAGACGGCG TGGTGGNCGG TCAGAGGGGC	240
TCCTCACTTC CCAGTAGGGG TGGCCGNGCA GGNGGTGCCC CNCACCCCCC GGGCGGGGTG	300
GTTNGTCCNN CCGGNGGGNT GCACNCCCC CACCCCTCCC CNCTCTNCTA CTGGCGGTCTG	360
TNTATTNCAN NATCTTTAAG CA	382

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGATCCAAAG GAAGTTAGAG GCCAGCTCAG TCTACACCTG CTA CTGNTCA GTGCCCACCC	60
GGTCAAGGGA GACCAACACA TGGTAAAGGT CAAGGGCTTC TTGGAAGGCA GTCAGCAGCC	120

TGTGCAAGAT GTTCTCCACA CTGCTCAGNT TAAGGGGAGC TGGGGGCAGG ACCTCAGCTG	180
GNATCTCTGC TTCACCACTG TCCAGGGGTT GCACAATTCT TGTTTACTCG TAGGATATTT	240
AATCTTGNN GGTGCTATCA TAAATGGGAC TTATCCNCTN ATTATGTTTT CTTACTAGTT	300
GTTTATGTGA AGGTTATTGA TTTGGGTTTC ACTTTATTTN GTGGNAATGG AGTTTCACTC	360

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 208 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AATGTCACGG ATTCCTTTAG GTAGNTACAC CCATCAACCT TTTTGAGAAT AAAATGAATT	60
GAGAGTGTTA CAGTCTAATT CTATATCACA TGTAACTTTT ATTTGGATAT ATCAGTAATA	120
GTGCTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GNGANAGAGT CTCGCTCTGT	180
CGCCAGGTTG GAGTGNAATG GTGCGATC	208

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 470 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AACAAGGTTT CTCGGTCGGC GGTGAATATA CCGGGGCGTC GATATTTGTT GCGGAATACT	60
CCCCTGACCG TAAACGTGGC TTTATGGGCA GCTGGCTGGA CTCGGTTCT ATTGCCGGGT	120
TTGTGCTGGG TGCGGGCGTG GTGGTGTTAA TTTCGACCAT TGTCGGCGAA GCGAACTTCC	180
TCGATTGGGG CTGGCGTATT CCGTTCTTTA TCGCTCTGCC GTTAGGGATT ATCGGGCTTT	240
ACCTGCGCCA TGCCTGGAA GAGACTCCGG CGTTCCAGCA GNATGTCGAT AAAGTGAAC	300
AGGGCGACCG TGAAGGTTTG GAGGATGGCC CGAAAGTCTC GTTTAAAGAG ATTGGCACTA	360
AATACTGGNG CAGNCTGTTG AATGTTTGGG CTTGGTAATT GGCAACCAAC GTGATTACTA	420
NATGTTGGTG ACCTATATTG CCGAGTTATT GGCGGATAAC CTGAATTATC	470

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 440 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TAATTATATT GAAATGCTTC TCNTCTAGGT CATCCATGNC TGGNTTATTA TATCATCTCT	60
ATTGNTGNTG CTCTTTTTTA CATNCATTTA CTTGGGGTAA GTTGTGAAAT TTGGGGTCTG	120
TCTTTCAGAA TTAACACCT NNGTGCTGTG TAGCTATCAT TTAAAGCCAT GTACTTTGNT	180
GATGAATTAC TCTGAAGTTT TAATTGTNTC CACATATAGG TCATACTTGG TATATAAAAAG	240
ACTAGNCAGT ATTACTAATT GAGACATTCT TCTGTNGCTC CTNGCTTATA ATAAGTAGAA	300
CTGAAAGNAA CTTAAGACTA CAGTTAATTC TAAGCCTTTG GGGAAGGATT ATATAGCCTT	360
CTAGTAGGAA GTCTTGTCN ATCAGAATGT TTNTAAAGAA AGGGTNTCAA GGAATNGTAT	420
AAANACCAAA AATAATTGAT	440

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AAACAAAGC CTCTTGAGGT TCTGAAAAGG GAAAGAAAAA CAGAACTTTG TGCACTACAA	60
TTATACTGTT ATAAAAACA CTTCCATAGA TTACATTAAG CAGAAACAAA CCTTTCTTTC	120
ATGTGTTCTC CTCCAGGCCA AGCTGTCTAA GGACCGCAAA GGCTGTTGTC ACTTGCAGGC	180
TCCCAGATTA GGTCTGAAAT AGGATTTTAC CAGGTCATCC ATTGTTAGTT AAATCCTAGT	240
AAATTCATTT ANACCAATCA AATACTTATA AGACCAATTT GTAAACCAGG AATGTATTAA	300
TTTGTCACGA CTTTCAACTA ACTGACAAAT TTACTATAAG CTCAAGGTAG GACTCTTTAG	360
CAATAAGTAG GAACCGCCTG AGACAACCAA ACATTTTCAA CCCACAAANG ATACTTTAAT	420
GACTTTCTGA TTNCCAGCA AAAGGGGGG	449

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGATCCGCCC TCCTCGGCCT CCCAAAGTGT TGGGATTACA GCGTGAGCC ACCGCACCTG	60
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GCTTTTTTTTT	TTTTTTTTTTT	TGGNGGAGAC	AGAGTCTTAC	TCTGTTGCCC	AAGCTGGAGT	120
GCAGTGGTGC	AATCTTGGTT	CACTGNAACC	TCCACCTCCA	GAGTTCAAGC	AATTCTCTGC	180
CTCAGTTTCT	GGAGTAGCTG	GGATTACAGG	TGCCTGCCAT	CACGCCTGGC	TAAATTTGGN	240
ATTTTTTTTTT	AGTAGAGACA	GGGTTTCACC	ATGTTGGCCA	GGCTGGTCTT	GAACTCCTGA	300
CCTTGTGATC	CACCAGCCTC	GGCCTCCCAA	ATTGNTGGGA	TTACAGGCGT	GAGCCACCAC	360
AACCAGGCTA	AAGTTTTAAA	ACATGCCAAG	TGTATTTACA	TAATGCGATA	CGANTTATGT	420
ACATA						425

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 386 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGATCCGCCC	GCCTTGGCCT	CCCAAAGTGC	TGGGATTACA	GGCATGAGCC	ACCGCTCCTG	60
GCTGAGTCTG	CGATTTCTTG	CCAGCTCTAC	CCAGTTGTGT	CATCTTAAGC	AAGTCACTGA	120
ACTTCTCTGG	ATTCCCTTCT	CCTNNTGTAA	AATAAGCATG	TTATCTGTCC	NNCCTGCCTT	180
GGGCATTGTG	ATAAGGATAA	GATGACATTA	TAGAATNTNG	CAAATTTAAA	AGCGCTAGAC	240
AAATGATTTT	ATGAAAATAT	AAAGATTAGN	TTGAGTTTGG	GCCAGCATAG	AAAAAGGAAT	300
GTTGAGAACA	TTCCNTTAAG	GATTACTCAA	GCTCCCTTTG	GTGTATATCA	GNNGTCANNA	360
CNTATCTTNG	GGGCTGAAAA	ATGTTT				386

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 224 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAAAGGGAA	AGAAAAACAG	AACTTTGTGC	ACTACAATTA	TACTGTTATA	AAAAACACTT	60
CCATAGATTA	CATTAAGCAG	AAACAAACCT	TTCTTTCATG	TGTTCTCCTC	CAGGCCAAGC	120
TGTCTAAGGA	CCGCAAAGGC	TGTTGTCACT	TGCAGGCTCC	CAGATTAGGT	CTGAAATAGG	180
ATTTCAACCAG	GTCATCCATT	GTTAGTTAAA	TCCTAGTAAA	TNCA		224

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 440 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGATCCGCCC TCCTCGGCCT CCCAAAGTGT TGGGATTACA GCGTGAGCC ACCGCACCTG	60
GCTTTTTTTTT TTTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCCC AAGCTGGAGT	120
GCAGTGGTGC AATCTTGGTT CACTGCAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC	180
CTCAGTTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGN TAAATTTGGG	240
ATTTTTTTTT AGTAGAGACA GGGTTTCANC ATGTTGGCCA GGNTGGTCTT GGA CTCTCTGA	300
CCTGGTGAAC CACCAGGCTC GGGCTCCAAA TTTGGTTGGG ATTACAGGGG GTNAANCAAC	360
CACAACCCAG NCTAAAGTTT TNA AACATN CAAAGTGTTT TAA AATNATG NGATACGATT	420
TATTGTACAA TTAATTTTAT	440

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 448 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTACTCCTTG CCATTTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTGTTTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA	180
TATTTGCGGN TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTTCTGTGT CCACATCTAA CAAAGTCAAG ATCCCCGGCT GGACTTTTGG	300
AGGTTCCCTC CAAGTCTTCC TGACCACCTT GCACTATTGG ACTTTGGNAA GGAGGTGCCT	360
ATAGAAAACG ATTTTGGAAC ATA CTTCATC GCAGGGGGAC TGTGTCCCCC GGTGGCAGAA	420
NCTACCAAGA TTTGCGGGNC GAGGTCAA	448

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTTNAGTAA AATAAGNATG TTATCTGNCC GCCCTGCCTN	180
GGNNATTGNG ATAAGGAT	198

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGCAGTGAG CCGTGATTGC ACCACTTTAC TCCAGCCTGG GCAACAAAAT GAGACCCTGG	60
CTCAAAAACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTAAAGGGAA GTATTAAATA	120
AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGATA TTAATATCTA	180
ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTNTTGG TGAAAATTAT TGTACATCTT	240
TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT TGCTGTGGAC	300
TACATTACTG TTGCACTCCT GATCTGGAAT TTTGGGTGTG GTGGGAATGA TTTCCATTCA	360
CTGGAAAGGT CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCTCATGGNC	420
CTGGTGTTTA TCAAAGTACC TCCCTGAATG GACTGCGTGG GTCATCTTGG NTGTGATTCA	480
GTATATGGTA AAACCCAAGA	500

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTGCAGCCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCACC ATGCCCGGCT AATNGNTGTA TTTTCTGTAG ATACGAGGTN	120
TNGCCATGTT GCCCAGGCTG GTCTTGAAC TGGGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCCC AGCCGAAATC TTCAAATGAA	240

AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCCTGTNA	360
CAAAACAAAT TATCAGTCTT GGGGTTTNAC CATATACTGA AATCACAGGC AAGATGAGCC	420
ACGCAGTCCA TNCAGGGAGG TACTGGATAA CACCAGGGNC ATGAGGGACT AATCATAATG	480
AGATATGCTG CTGGAGTCGA	500

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGCAGGATG AGAGCGATCT CTTNTTNCAT TTCCTGCGCT ACGCGCTGCG GGCGACCAAA	60
TTCTTTTCGCC ATAATAAATT CTCCTGACNA AAAAGGGGCT GTTAGCCCCT TTTTAAAATT	120
AATTTTCAGGT GGAAGGGCTG TTCACGTTGA CCTGATAAGA CGCGCCAGCG TCACATCAGG	180
CAATCCATGC CGGATGCAGC GTAAACGCCT TATCCCGCAT GGAACCCTAA AAACCTTAAG	240
CAATGGTACG TTGGATCTCG ATGATTTCTGA ATACTTCGAT CACATCGNCA GTGCGGACGT	300
CGTTGTAGTT CTTAACGCCG ATACCACATT CCATACCGTT ACGGGACTTC GTTAACGTCA	360
TCTTTGGAAG CGGGGCAGGG ACTCCAGCTC GNCTTCGTAG ATAACCACGT TGGCACGCAG	420
GAACGCGGGT CGGGTTGTGA CGTTTAAACAC AACTTCCGGG TAACCATACA GGCTGNGATG	480
GNACCAAATT TCGGGGGATT TGGACAAGTC AAGAACTTCC CGCCAGACCG ATAATCTTGT	540
TGTTCACTTC	550

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 541 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTTA	120
TNTTGTATTAT GTTGTCTCCC CCACCCCCAC CAGTTCACCT GCCATTTATT TCATATTCAT	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTTCCT TCGTTAATTC	240

CTCCCTACCA CCCATTTACA AGTTTAGCCC ATACATTTTA TTAGATGTCT TTTATGTTTT	300
TCTTTTNCTA GATTTAGTGG CTGNGTTGTG TCCGAAAGGT CCACTTCGTA TTGCTGGTTG	360
AAACAGCTCA GGAGAGAAAT GAAACGCTTT TTCCAGCTCT CATTACTCC TGTAAGTATT	420
TGGAGAATGA TATTGAATTA GTAATCAGNG TAGAATTTAT CGGGAAGTTG AAGANATGTN	480
ACTATGGCAA TTTCANGGNA CTTGTCTCAT CTAAATGAN AGNATCCCTG GACTCCTGNA	540
G	541

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 241 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

NNCCNCNCN NNNNNNTTN NTNTTGCCCG ATAACATAG GGNGACTTGG AGATCCACCG	60
CGGTGGCGGN CGNTCTAGAA CTAGTGGATC CCCCGGGNTG CAGGACCCAA CGCTGCCCGA	120
GATGCGCCGC GTGCGGTTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT	180
GGTTTGCGCA TTCACAGTTC TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA	240
T	241

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCCCNCC NNNNNTTTTN NGCAGCCCGT AATTACCCTC ACTNCCGGGA ACAAAGCTG	60
GGTACCGGGC CCCCCCTCGA GGTGACGGT ATCGATAAGC TTGATATCGA ATTCCTGCAG	120
TGTTTAAAAA ATAAAATAAA CTAAAAGTTT ATTTATGAGG AGTACACTGC TTTCTTGTA	180
ACACATGTAC AAGCCATATA ATAGAGTTCA TTTTACCC TAGTTACGGA AACACTAGAA	240
AGTCTTCACC CGGCCAAGAT AACACATCTT TAGTAAAAAT AGCAAGAAAT ATTTTATGGG	300
TTGTTTACTT AAATCATAGT TTTCAGGTTG GGCACAGTGG NTCATGCCTG TAATCCCAGC	360
ACTTTATGCG GNTGAGGCAG GCAGATCAGT TGAGGTCAGA AGTTTGGAGA CCAGNCTGGG	420
CAATGTGGNA AAACCTCATC TCCACTAAAA ATACAAAAAT TAGNCAGGCA TGGTGGTGCA	480

CACATGTAAT TCCAGNTACT TGGGGAGGCT GAGACAGGAG GATCGNTTGA ACCTAGGGAG	540
GGAGGAGTTG GAGTGAGCTA ATGTCAATGC ACTCTTGGTT GGGGCGANAG AGCAAGATCT	600
TTCTTCCAAA AAAAAAAAAA AAAAAAAGC CAGGTGNGGN GGTCAAGGCT GTAATCCAGA	660
ATTNGGGAGG CCGNGGAGGN NATCANTGNG GNAGGNGTCA AGNGGGGCNG GCCACATGGG	720
GAACCCGTTN TTNTTAAATN AAAATTAGCC GGGGNGGGGG AGGACTNTAT CCNGTTCCGG	780
NGGTGNGGAG GATCNTTATT NTGGNGGAGG GTGGATGNNC CAGTTGACNC CCCC	834

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 838 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTGGGCNCNC GCCCCTTAAN TTTTATNGN TTNCTANAAA AANANNNGGC NCNNTAAAAT	60
ATATTTTTTN TTGTGACCCC TTTTAAAAGG GACCCNCTAA AAAATTTTNT GGTNNNTTN	120
GATTTANGTG GGTGNTTTTN TTATATTTTT GNGAGNNTC TGTAGTCNTC NCCCTCAAAC	180
ANNTCNTACN ATNGGNANCG TGA CTCTGTC NTTNGTNANN NTCGNTNTCN NGTNATTCNA	240
GGNNCCTCGC GCNNCNCGGG CNNNGTTTTT TTTNNCNNTT TTTAAGCCNA ANNCTCAGTA	300
NCNTCCAACG GNGCTNNGAC ANNNGNNNCT NTCGNGGGTN CCCTCTNTNT NGNNCNNGGC	360
TNNNGNNNNC NGNCNGCNGN GCCNTGCGNN NNGNNNGNGG NNGNTNNCA TANGGATNGN	420
GNTGCTCNC NCNNGNGTNN TNAGTAGGNA NTTTTNTNNT ACTTGCCNNC NNNTNGCTGC	480
GAGNANAGCN ANNTNGNNGN AGNGNNGNTG CGCGGANNTT CCCCTGATNA NCTCGAGCNG	540
NTTACNGGNG CNNCCTNGAA NAAGNGNNGT ANNGTGCCGA GNCGCTANNC TGAGCCTGAG	600
TNTCGACNGG NATNGTGNNT CNTACNGTTA NGGGNNGCNN GANCGGGNTG ANTCNCCGGN	660
NGANCNAGCG ACTGCCTNTC ANGCGAANCG TNTCANGNNN GTAGAGCANA GGGTNANNNG	720
TCNNNNAAGC NTNNAGTGAN TGTCNTNACN NGTGANTTAC GGCNTAGNCT TGATNTNNAN	780
NCGAGGNNNN ATNNANNNTT GGANANTTNN TNNNTCNCN TCGCGGNGNG NCNNGCCG	838

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 803 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATTTCGCGCGT AGCCCGATAA CTATAGGGCG ACNTGGAGNT CCACCGCGGT GGCGGCCGCT	60
CTAGNAACTA GTGGATCCCC CGGGCTGCAG GAATTCACGG ACTAATCCTC TACAGATCTT	120
GCTGGAGTGG CCTTTCAGCC TTTTGTGACT GTTTGTAGTG AAATGTACAC ACAAGCCTAC	180
AAGGCAGCCC AGATGTACCA TAACTGTGGG AAAATTAAAA AAAAAAAAAAC ACAGAACCTC	240
TCTATGTTGC CCATGCTGGA CTCAAACCTCT TAGACAAGCA ATCCTCGTAC CTCAGCCTCC	300
TGAGTTCCTG AGTAGCTGGG ACTACAAGCA TGCACCACCA TGCCAGGCTA TGAGAAAGTT	360
CTTTTTATTG ATCCAGACCT TATTGCCTGG TAACTTCCAC CACTGTTCTC AGCTCTGNTC	420
TCTGGTCCTA ACAGAGGAAA ATCTTGACCC CACACCTAGT GCAACTGGAT AGCTTATNGT	480
TGGGCTNGTG TTTCTCTAT TCTGGGTCCA CCCTAAAATC CNATAGATAC TCCAACCTGCT	540
CANAGNAAAC CAAGCTCTCT CTCTNNCTTN CTTTCTTNNN CTCTATTNAT TNATGGGNNA	600
TNATTNATTN NGGGGATGGN GTTCGGTCGC CGCCCGGCTG GNGTGAAATG GGGGAGGCAA	660
TCAATTTAAC CCCACCCNGG GTCCAGGGAT CTCGTTNAAA CCGNNNNNNN NNNNNNNNA	720
NGNCCNNCNC NNNCCNNTNN NNGGTTTNN NNGNNNNGG NNNCCNNNNN NANNNNNNTN	780
NNNCCNCCNA NNNTNCNNNN CCC	803

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CNNNNNNNCC CNNTNATTNT ACGCCAGCCG CGTAATTAAC CCTCACTAAA GGAACAAAA	60
GCTGGGTACC GGGCCCCCCC TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCA	120
ACTCCTCACT TGCCAGATGT GACCTTAAGC AAGTGAACCT CTGTGTGCCA CACTGTTTTTC	180
ATCTGTAAAA GGATAAAGGG AATATCATAA ATTAGNTTGT TAAGCCTTAG TTTAATAATG	240
TCTCTAAGTT TTACATATAA GTAGACAGTG TCTTTCTTGT TTAGTGAATA ATCATTCTTA	300
TTATTTAATA GTATCTCTAC TAAATTTATT GTGTAAGATT ATACTAATCT TGTTTAGTGC	360
GTGGTAATCA CTTCTGCTCA TATTTAACCT ATAAGCATAA TATAGTTTAT TTATATACCA	420
NTTATTTATT TTATTTTATT TGNNGAGATG CAGCTTGCT TTNCAACCC AGGGNTGNGG	480
NGNAGNNGNG NAANCTTGNT TCACTGNAAC CNCCACCNC CAGGTNCAAG NGATTCTCCT	540
GNTCAAGCCN CCTNAGNAGN TGGNATTACA GNACGANTAC ANNCCAGNTA NNNNGGNTNT	600
NNGNTNGNNA GGNNNCACAN NNGNCAGGTN NNTCGNCTCC NNGCCANTNA CTNNNNCCAN	660

CCCCNNNGNN NNNNATANAG NATNANCANN NNCCNCNNNN NCNNNNNNNG GNGGANCCN	720
NNTNGCNGNN ANNGNNANN NNTNNNNNNN NNGGNCNNNG NNNNNNNNCC NNNNNNCCCC	780

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 803 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

NNNNNNNNNC CNNNNNNTTC GNNCGTAACN CGANTCACTA TAGGGCGACT TGGAGCTCCA	60
CCGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGGG CTGCAGGAAT TCGATATCAA	120
GCTTTNGTGT GTAAAAAGTA TTAGAATCTC ATGTTTTTGA ACAAGGTTGG CAGTGGGTTG	180
GGAGGAGGGA TTGGAGATTG ATGCGATAGG AATGTGAAGG GATAGCTTGG GGTGGATTTT	240
ATTTTTTAAT TTTAATTTTT ATTTNTTGAG ATGGAGTCTT GCTCTGTCTC CCAGGCTGGA	300
GTGCAGTGGT GTGATCTCAG CTCACGGGTT CAAGCGATTC TCCTGCTGCA GCCTCCCGAG	360
TAGCTGGGAT TACAGGAGCG CGCCACCACA CCCGGNTAAT TTNNTTGAT TTTTAGTAGA	420
GACGGGGTTT CACCATGTTG GTTAGGCTGG TCTAGAACTC CCAACCTCAT GATCCGCCTG	480
CTTCGGCCTC CCAAAGTGCC GGAATTACAG GCGTGAGCGA CTGCACCCGG CCGCTTGGGG	540
GTGGATTTTT AAAGAAATTT AGAAGAATGT AACTTGGCCA GATACCATGT ACCCGTTAAT	600
TCATTTNCGG TTTTTTGGAT ACCCATTTTG NNATTCTCCC NCCACTGGAT AAATAAGGN	660
GGTTCATTNT NGNTTAGTTT GGGTNTTTTT NAGTGTGGNT TCTGCTTATN ATTAGAATGG	720
NCTNCTTTNC CAANCTGGAA AGGGAGGAGT TAAAATCANT ACCAGANCA GAAATTCTTT	780
TCANTTGTTG CNCNAGAAAT GCC	803

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 819 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TNCCNNNNCN NNNNNAATTT TNGCAGNCGC GTAATTAACC TCACTAAAGG GAACAAAAGC	60
TGGGTACCGG GCCCCCCTC GAGGTCGACG GTATCGATAA GCTTCCCTCC CCTTCCTCAG	120
CTCTGGCGAC CCTGCGCTGT GGTGGTTCTC CAACCACACT CATTCTCCTC AGCTGGCTCC	180
TTGCTCTTCT TCCACCCCT CGTTGGAAGT GTTCCTAAGT GTTTGGCTTG GCCTCCTCTT	240



CCCCTTCCTT	AGNTTAGACT	TCTCCACTGC	TCCAACATCA	ACTGGAAATC	TATGGAATTG	300
ATTCTGTGTT	TCAGCTCCAG	TCCTGTTTAC	AGGGCATTTT	CACCTGCTGG	CACTTCCAAA	360
GTGACACTTC	CAAACCACTT	CCTCGCCCTC	CTCTCTAAAC	CAGGTCTTTC	TTCCTAACTT	420
CCTTATTTCT	GAGAATGTCT	CTGNCATGTT	CTAAACTGAA	AACTCCTAGT	CAACTNCACA	480
CTTTATTCCC	TGGATCCTCA	ATTGGGTTCC	CATGTNCCGT	TAGTGTTTCT	TGGTAAGNCT	540
CTGCCANCAC	CGNAGGATCG	ACTCTAATCA	CATCTCAACT	GAATTATGGN	AAAGTCAACT	600
CAATTCTCTC	AACCATCCCA	GGCTCCACTA	TGGNTAATAT	GCTAAGGAGA	GCTGACCCAA	660
CGGGGAGAAG	ATCTGNNGGG	GAGGAGAGAA	ACAAAGNTAA	TGGAATNATT	CTCGAAAAGC	720
CCACAAGGNG	AAGGATAACC	CNCTTCNCNT	CGAAAGAGGG	GGGATCGCCA	GATNTCGCGC	780
CCGGAAAGAA	ACCGGGGNGA	GGGGGTTACA	NTGTAAGNC			819

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 796 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TNTTGGCTGG	TACTGCTTGA	GCAACTGGTG	AAACTCCGCG	CCTCACGCCC	CGGGTGTGTC	60
CTTGTCCAGG	GGCGACGAGC	ATTCTGGGCG	AAGTCCGCAC	GCCTCTTGTT	CGAGGCGGAA	120
GACGGGGTCT	GATGCTTTCT	CCTTGGTCGG	GACTGTCTCG	AGGCATGCAT	GTCCAGTGAC	180
TCTTGTGTTT	GCTGCTGCTT	CCCTCTCAGA	TTCTTCTCAC	CGTTGTGGTC	AGCTCTGCTT	240
TAGGCATATT	AATCCATAGT	GGAGGCTGGG	ATGGGTGAGA	GAATTGAGGT	GACTTTTCCA	300
TAATTCAGGT	GAGATGTGAT	TAGAGTTCGA	TCTGCGGTGG	TGGCAGAGGC	TTACAAGAAA	360
CACTAACGGG	ACATGGGAAC	CAATTGAGGA	TCAGGGAATA	AAGTGTGAAG	TTGACTAGGA	420
GGTTTTTCAGT	TTAGAACATG	GCAGAGACAT	TCTCAGAAAT	AAGGAAGTTA	GGAAGAAAGA	480
CTGGTTTAGA	GAGGAGGGCG	ANGAAGTGGT	TTGGGAAGTG	TCACTTTGGG	AAGTGCCAGC	540
AGGTGAAAAT	GCCTGTGACA	GGATGGAGCT	GAAAACAGGA	TCAATTCCAT	AGATTCCAGT	600
TGATGTNGGA	GCAGGGGAGA	AGTCTTAGCT	AAGGAAGGGG	AAGAGGAGGC	CAAGGNAACA	660
CTTAGGACAA	TTGNAACGAN	GGGGGGGGAG	AAGAGNAAGG	GCCACTTAGG	GGAATAATNT	720
GGTGGGGGAC	CCCCAAGNNA	GGGCGCANNN	TTAGGAGGGG	GGGANNTCAN	AGGAAAGTGG	780
AAGNTTGGGT	TTANCT					796

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 802 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTTCGTCGTA NCCCGATNAC TATAGGGCGA CTTGGAGCTC CACCGCGGTG GCGGNCGCGG	60
GCAGGGNCCG GNCCTTTGTG GCCGCCCGGG CCGCGAAGCC GGTGTCCTAA AAGATGAGGG	120
GCGGGGCGCG GNCGGTTGGG GCTGGGGAAC CCCGTGTGGG AAACCAGGAG GGGCGGCCCCG	180
TTTCTCGGGC TTCGGGCGCG GCCGGGTGGA GAGAGATTCC GGGGAGCCTT GGTCCGGA	240
TGCTGTTTGC TCGAAGACGT CTCAGGGCGC AGGTGCCTTG GGCCGGGATT AGTAGCCGTC	300
TGAACTGGAG TGGAGTAGGA GAAAGAGGAA GCGTCTTGGG CTGGGTCTGC TTGAGCAACT	360
GGTGAAACTC CGCGCCTCAC GCCCCGGGTG TGTCTTGTC CAGGGGCGAC GAGCATTCTG	420
GGCGAAGTCC GCACGCCTCT TGTTCGAGGC GGAAGACGGG GTCTTGATGC TTTCTCCTTG	480
GGTCGGGGAC TGTCTCGAGG CATGCATGTC CAGTGA	540
TCTCAGATCT TCTACCGNG GTGGGCAACT CTGTTTAGGC ATATTATCCA TAGNGGAGGC	600
TGGATGGTTG AAANAATTGA GGTNATTTTC CATAATCAAG TGAAATTTGA TAGAGTCCGN	660
CTTTNNGGGT GNAAGGGTTA AAAAAAATA ACGGAAATGG AACAATGAGG TCAAGGATTA	720
GTTGAGTTGN TAGNGGTTCA ATTAGANATG AAGGNATCTA AAATAGGAGT AGAGAANNNG	780
TTNAAAGAGG GAAAATTTTG CC	802

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 793 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATATGCAGCC GCGTAATTAA CCTCACTAAA GGAACAAAA GCTGGGTACC GGGCCCCCCC	60
TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCT GCAGCCCGGG GGATCCGCCC	120
CGCGGCCTCC CAAAGTGCTG GGATTACAGG CGTGAGCCAC CGCCCCGGGN CTCACATTTT	180
ATTTCTATTG GCTAGCGCTG CTCTAAATCT TCTGTTTCCTT CTGCTACACC AGGCCTAACA	240
CTCAAAATCC CTGCCAACCT TTTCTTCCTT GAAGCTTCCC TCCCCTTCCT CAGCTCTGGC	300
GACCCTGCGC TGTGGTGGTT CTCCAACCAC ACTCATTTCTC CTCAGCTGGC TCCTTGCTCT	360
TCTTCCACCC CCTCGNTGGA AGTGTTCTTA AGTGTTGGC TTGGCCTCCT CTTCCCTTC	420

CTTAGCTTAG ACTTCTCCAC TGCTCCAACA TCAACTGGAA ATCTATGGAA TTGATTCTTG	480
TTTCAGCTCC AGTCCTGTTC ACAGGGGATT TTCANCTGGT GGCATTTCCA AAGTGAAATT	540
CCAAACCACT TCCTCGGCCT CCTCTTCTAA ANCAGGTCTT TCTTCCTAAC TTCCTTATTC	600
TTGAGAATGT CTCTGCATGT TCTTAAANTG AAAACTCCTA GTCAAATTCA AATTTATCCC	660
TGATCCCAAA TGGTCCCATC CCCGTAGGGT TTNTGTAGCC TGCACACCGA GGTCGGANTT	720
TATNNATTCA CCGATTATGG AAAGTAACCA ATCTTNACCA NCCAGCTCAT TTGTTNTNTG	780
CTAAGAGGGT NCC	793

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAGTCATGG ATTCCTTTAG GTAGCTACAT TATCAACCTT TTTGAGAATA AAATGAATTG	60
AGAGTGTTAC AGTCTAATTC TATATCACAT GTAACCTTTA TTTGGATATA TCAGTAATAG	120
TGCTTTTTTCN TTTTTTTTTT TTNTTTTTTT TNNTTTTNGG GGANAGAGTC TCGCTCTGTC	180
GCCAGGTTGG AGTGCAATGG TGCGATCTTG GCTCACTGAA AGCTCCACCN CCCGGGTTCA	240
AGTGATTCTC CTGCCTCAGC CNCCCAAGTA GNTGGGACTA CAGGGGTGCG CCACCACGCC	300
TGGGATAATT TTGGGNTTTT TAGTAGAGAT GGC GTTTCAC CANCTTGGNG CAGGCTGGTC	360
TTGGAACTCC TGANATCATG ATCTGCCTGC CTTAGCCTCC CCAAAGTGCT GGGATTNCAG	420
GGGTGAGCCA CTGTTCTTGG	440

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTTAGTCTGT NTCGTAGTCA TATTAATTGT AAGTNTACAC TAATAAGAAT GTGTCAGAGC	60
TCTTAATGTC AAAACTTTGA TTACACAGTC CCTTTAAGGC AGTTCTGTTT TAACCCCAGG	120

TGGGTAAAT ATTCCAGCTA TCTGAGGAGC TTTTNGATAA TTGGACCTCA CCTTAGTAGT	180
TCTCTACCCT GGCCACACAT TAGAATCACT TGGGAGCTTT TAAAACTGTA AGCTCTGCCC	240
TGAGATATTC TTACTCAATT TAATTGTGTA GTTTTTAAAA TTCCCCAGGA AATTCTGGTA	300
TTTCTGTTTA GGAACCGCTG CCTCAAGCCT AGCAGNACAG ATATGTAGGA AATTAGCTCT	360
GTAAGGTTGG TCTTACAGGG GATAAACAGA TCCTTCCTTA GNCCCTGGGA CTTAATCACT	420
GAGAGTTTGG GTGGNGGTTT NGNATTTAAT GAC	453

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GACACACATT CACACATAAT TATGAAAGCA TTTTCAGGCA AAACCTCAATC ACAAGTCTGG	60
GTTTTTAACA TAGTTAACTG AATATTTCCC TTGGGGGGTT AAATTTTAGA ACAGACGTNC	120
ATNCAATCTG GAAGAAGAGC TATGAAAAAA ACCTAGCTTG GTTNGGTTTC ATAGGGTNCA	180
TTATGNACAC ATTGTTATTT TATCCCTTAA TNCTAGTAAA GAAATAGAAT CTGAAAATAA	240
GTAAAACTAC TTGGAAAAAA NTTAAAGAT ACAGAAATTT CTATCTTAAA TGATGTGTGG	300
GCCNCTGTGA TTTTAGTNGG GNTGGTTAAA ANCCAGAGG TGAAGAGNAT NCTCTATGCT	360
GTGNGGGGG	369

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTCATCATG CTTACGGGG GAGGCTGTGC GGAAGAATG CTCCCACACA GNATAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCCCG CACAGCATAG AGAAGCCCC GCACAGCATA	120
GAGAATGCCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT	180
CTGGGTTTTT AACCAGCCAA ACTAAAATCA CAGAGGSCMA CACATCATTT AAGATAGAAA	240
TTTCTGTATC TTTTAATTTY TTTCMAAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT	300
ACTAGAATTA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA	360
GCTAGGTTTT TTTCATAGST CTTCTTCCAG ATTGAATGAA CGTCTGTTCT AAAATTTAAC	420

CCCCCAGGGA AATATTCAGT TAACTATGTT AAAAACCCAG ACTTGTGATT GAGTTTTGCC 480  
 TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC 516

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTATAATGCA GGTGCTATAA GGTGAGCATG AGACACAGAT CTTTGCTTTC CACCCTGTTC 60  
 TTCTTATGGT TGGGTATTCT TGTCACAGTA ACTTAACTGA TCTAGGAAAG AAAAAATGTT 120  
 T 121

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TGGAGACTGG AACACAAC 18

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGTGGCCAG GGTAGAGAAC T 21

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATCTCCGGCA GGCATATCT

19

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGAAATCACA GCCAAGATGA G

21

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CCATAGCCTG TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CCATAGCCTA TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2791 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TGGGACAGGC	AGCTCCGGGG	TCCGCGGTTT	CACATCGGAA	ACAAAACAGC	GGCTGGTCTG	60
GAAGGAACCT	GAGCTACGAG	CCGCGGCGGC	AGCGGGGCGG	CGGGGAAGCG	TATACCTAAT	120
CTGGGAGCCT	GCAAGTGACA	ACAGCCTTTG	CGGTCCTTAG	ACAGCTTGGC	CTGGAGGAGA	180
ACACATGAAA	GAAAGAACCT	CAAGAGGCTT	TGTTTTCTGT	GAAACAGTAT	TTCTATACAG	240
TTGCTCCAAT	GACAGAGTTA	CCTGCACCGT	TGTCCTACTT	CCAGAATGCA	CAGATGTCTG	300
AGGACAACCA	CCTGAGCAAT	ACTGTACGTA	GCCAGAATGA	CAATAGAGAA	CGGCAGGAGC	360
ACAACGACAG	ACGGAGCCTT	GGCCACCCTG	AGCCATTATC	TAATGGACGA	CCCCAGGGTA	420
ACTCCCGGCA	GGTGGTGGAG	CAAGATGAGG	AAGAAGATGA	GGAGCTGACA	TTGAAATATG	480
GCGCCAAGCA	TGTGATCATG	CTCTTTGTCC	CTGTGACTCT	CTGCATGGTG	GTGGTCGTGG	540
CTACCATTAA	GTCAGTCAGC	TTTTATACCC	GGAAGGATGG	GCAGCTAATC	TATACCCCAT	600
TCACAGAAGA	TACCGAGACT	GTGGGCCAGA	GAGCCCTGCA	CTCAATTCTG	AATGCTGCCA	660
TCATGATCAG	TGTCATTGTT	GTCATGACTA	TCCTCCTGGT	GGTTCGTGAT	AAATACAGGT	720
GCTATAAGGT	CATCCATGCC	TGGCTTATTA	TATCATCTCT	ATTGTTGCTG	TTCTTTTTTT	780
CATTCAATTA	CTTGGGGGAA	GTGTTTAAAA	CCTATAACGT	TGCTGTGGAC	TACATTACTG	840
TTGCACTCCT	GATCTGGAAT	TTTGGTGTGG	TGGGAATGAT	TTCCATTAC	TGGAAAGGTC	900
CACTTCGACT	CCAGCAGGCA	TATCTCATTA	TGATTAGTGC	CCTCATGGCC	CTGGTGTTTA	960
TCAAGTACCT	CCCTGAATGG	ACTGCGTGCC	TCATCTTGCC	TGTGATTTC	GTATATGATT	1020
TAGTGGCTGT	TTTGTGTCCG	AAAGGTCCAC	TTCGTATGCT	GGTTGAAACA	GCTCAGGAGA	1080
GAAATGAAAC	GCTTTTTTCCA	GCTCTCATTT	ACTCCTCAAC	AATGGTGTGG	TTGGTGAATA	1140
TGGCAGAAGG	AGACCCGGAA	GCTCAAAGGA	GAGTATCCAA	AAATTCCAAG	TATAATGCAG	1200
AAAGCACAGA	AAGGGAGTCA	CAAGACACTG	TTGCAGAGAA	TGATGATGGC	GGGTTCAGTG	1260
AGGAATGGGA	AGCCCAGAGG	GACAGTCATC	TAGGGCCTCA	TCGCTCTACA	CCTGAGTCAC	1320
GAGCTGCTGT	CCAGGAACTT	TCCAGCAGTA	TCCTCGCTGG	TGAAGACCCA	GAGGAAAGGG	1380
GAGTAAAACT	TGGATTGGGA	GATTTTCATTT	TCTACAGTGT	TCTGGTTGGT	AAAGCCTCAG	1440
CAACAGCCAG	TGGGACTTGG	AACACAACCA	TAGCCTGTTT	CGTAGCCATA	TTAATTGGTT	1500
TGTGCCTTAC	ATTATTACTC	CTTGCCATTT	TCAAGAAAGC	ATTGCCAGCT	CTTCCAATCT	1560
CCATCACCTT	TGGGCTTGTT	TTCTACTTTG	CCACAGATTA	TCTTGTACAG	CCTTTTATGG	1620
ACCAATTAGC	ATTCCATCAA	TTTTATATCT	AGCATATTTG	CGGTTAGAAT	CCCATGGATG	1680
TTTCTTCTTT	GACTATAACC	AAATCTGGGG	AGGACAAAGG	TGATTTTCCT	GTGTCCACAT	1740

CTAACAAAGT CAAGATTCCC GGCTGGACTT TTGCAGCTTC CTTCCAAGTC TTCCTGACCA	1800
CCTTGCACTA TTGGACTTTG GAAGGAGGTG CCTATAGAAA ACGATTTTGA ACATACTTCA	1860
TCGCAGTGGA CTGTGTCCCT CGGTGCAGAA ACTACCAGAT TTGAGGGACG AGGTCAAGGA	1920
GATATGATAG GCCCCGAAGT TGCTGTGCCC CATCAGCAGC TTGACGCGTG GTCACAGGAC	1980
GATTTCACTG ACACTGCGAA CTCTCAGGAC TACCGGTTAC CAAGAGGTTA GGTGAAGTGG	2040
TTTAAACCAA ACGGAActCT TCATCTTAAA CTACACGTTG AAAATCAACC CAATAATTCT	2100
GTATTAACTG AATTCTGAAC TTTTCAGGAG GTACTGTGAG GAAGAGCAGG CACCAGCAGC	2160
AGAATGGGGA ATGGAGAGGT GGGCAGGGGT TCCAGCTTCC CTTTGATTTT TTGCTGCAGA	2220
CTCATCCTTT TTAAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA	2280
TTGCCTTTTG CAATTCTTCT TCTCAAGCAC TGACACTCAT TACCGTCTGT GATTGCCATT	2340
TCTTCCCAAG GCCAGTCTGA ACCTGAGGTT GCTTTATCCT AAAAGTTTTA ACCTCAGGTT	2400
CCAAATTCAG TAAATTTTGG AAACAGTACA GCTATTTCTC ATCAATTCTC TATCATGTTG	2460
AAGTCAAATT TGGATTTTCC ACCAAATTCT GAATTTGTAG ACATACTTGT ACGCTCACTT	2520
GCCCCCAGAT GCCTCCTCTG TCCTCATTCT TCTCTCCCAC ACAAGCAGTC TTTTCTACA	2580
GCCAGTAAGG CAGCTCTGTC TGGTAGCAGA TGGTCCCATT ATTCTAGGGT CTTACTCTTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTTAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
			20					25					30		
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
		35				40						45			
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu
	50					55					60				



Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys  
 65 70 75 80  
 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val  
 85 90 95  
 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln  
 100 105 110  
 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg  
 115 120 125  
 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val  
 130 135 140  
 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys  
 145 150 155 160  
 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe  
 165 170 175  
 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala  
 180 185 190  
 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val  
 195 200 205  
 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala  
 210 215 220  
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr  
 225 230 235 240  
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr  
 245 250 255  
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val  
 260 265 270  
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr  
 275 280 285  
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu  
 290 295 300  
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr  
 305 310 315 320  
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe  
 325 330 335  
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg  
 340 345 350  
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile  
 355 360 365  
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly  
 370 375 380  
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
 385 390 395 400  
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile

405	410	415
Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu		
420	425	430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala		
435	440	445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln		
450	455	460
Phe Tyr Ile		
465		

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1964 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCANACANC GGCAGCTGAG GCGGAAACCT AGGCTGCGAG CCGGCCGCCC GGGCGCGGAG	60
AGAGAAGGAA CCAACACAAG ACAGCAGCCC TTCGAGGTCT TTAGGCAGCT TGGAGGAGAA	120
CACATGAGAG AAAGAATCCC AAGAGGTTTT GTTTTCTTTG AGAAGGTATT TCTGTCCAGC	180
TGCTCCAATG ACAGAGATAC CTGCACCTTT GTCCTACTTC CAGAATGCCC AGATGTCTGA	240
GGACAGCCAC TCCAGCAGCG CCATCCGGAG CCAGAATGAC AGCCAAGAAC GGCAGCAGCA	300
GCATGACAGG CAGAGACTTG ACAACCCTGA GCCAATATCT AATGGGCGGC CCCAGAGTAA	360
CTCAAGACAG GTGGTGGAAC AAGATGAGGA GGAAGACGAA GAGCTGACAT TGAAATATGG	420
AGCCAAGCAT GTCATCATGC TCTTTGTCCC CGTGACCCTC TGCATGGTCG TCGTCGTGGC	480
CACCATCAAA TCAGTCAGCT TCTATACCCG GAAGGACGGT CAGCTAATCT ACACCCCATT	540
CACAGAAGAC ACTGAGACTG TAGGCCAAAG AGCCCTGCAC TCGATCCTGA ATGCGGCCAT	600
CATGATCAGT GTCATTGTCA TTATGACCAT CCTCCTGGTG GTCCTGTATA AATACAGGTG	660
CTACAAGGTC ATCCACGCCT GGCTTATTAT TTCATCTCTG TTGTTGCTGT TCTTTTTTTC	720
GTTCATTTAC TTAGGGGAAG TATTTAAGAC CTACAATGTC GCCGTGGACT ACGTTACAGT	780
AGCACTCCTA ATCTGGAATT TTGGTGTGGT CGGGATGATT GCCATCCACT GGAAAGGCCC	840
CCTTCGACTG CAGCAGGCGT ATCTCATTAT GATCAGTGCC CTCATGGCCC TGGTATTTAT	900
CAAGTACCTC CCCGAATGGA CCGCATGGCT CATCTTGGCT GTGATTTTCT TATATGATTT	960
GGTGGCTGTT TTATGTCCCA AAGGCCCACT TCGTATGCTG GTTGAAACAG CTCAGGAAAAG	1020
AAATGAGACT CTCTTTCCAG CTCTTATCTA TTCCTCAACA ATGGTGTGGT TGGTGAATAT	1080

GGCTGAAGGA GACCCAGAAG CCCAAAGGAG GGTACCCAAG AACCCCAAGT ATAACACACA	1140
AAGAGCGGAG AGAGAGACAC AGGACAGTGG TTCTGGGAAC GATGATGGTG GCTTCAGTGA	1200
GGAGTGGGAG GCCCAAAGAG ACAGTCACCT GGGGCCTCAT CGCTCCACTC CCGAGTCAAG	1260
AGCTGCTGTC CAGGAACTTT CTGGGAGCAT TCTAACGAGT GAAGACCCGG AGGAAAGAGG	1320
AGTAAACTT GGAAGTGGGAG ATTTTCATTTT CTACAGTGTT CTGGTTGGTA AGGCCTCAGC	1380
AACCGCCAGT GGAGACTGGA ACACAACCAT AGCCTGCTTT GTAGCCATAC TGATCGGCCT	1440
GTGCCTTACA TTACTCCTGC TCGCCATTTT CAAGAAAGCG TTGCCAGCCC TCCCCATCTC	1500
CATCACCTTC GGGCTCGTGT TCTACTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA	1560
CCAACTTGCA TTCCATCAGT TTTATATCTA GCCTTTCTGC AGTTAGAACA TGGATGTTTC	1620
TTCTTTGATT ATCAAAAACA CAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT	1680
TCCTGTGTCC TCAGCTAACA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCCGA	1740
GTCTCCCTAG CCACCCGCAC TACTGGACTG TGAAGGAAG CGTCTACAGA GGAACGGTTT	1800
CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA	1860
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GACCGTGGGC ATGGAGATTT	1920
ACCCGCACTG TGAAGTCTCT AAGGTAAACA AAGTGAGGTG AACC	1964

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2285 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCA CGAGGGCATT TCCAGCAGTG AGGAGACAGC CAGAAGCAAG CTTTTGGAGC	60
TGAAGGAACC TGAGACAGAA GCTAGTCCCC CCTCTGAATT TTACTGATGA AGAAACTGAG	120
GCCACAGAGC TAAAGTGACT TTTCCAAGG TCGCCCAGCG AGGACGTGGG ACTTCTCAGA	180
CGTCAGGAGA GTGATGTGAG GGAGCTGTGT GACCATAGAA AGTGACGTGT TAAAAACCAG	240
CGCTGCCCTC TTTGAAAGCC AGGGAGCATC ATTCATTTAG CCTGCTGAGA AGAAGAAACC	300
AAGTGTCGGG GATTCAAGAC CTCTCTGCGG CCCCAAGTGT TCGTGGTGCT TCCAGAGGCA	360
GGGCTATGCT CACATTCATG GCCTCTGACA GCGAGGAAGA AGTGTGTGAT GAGCGGACGT	420
CCCTAATGTC GGCCGAGAGC CCCACGCCGC GCTCCTGCCA GGAGGGCAGG CAGGGCCCAG	480
AGGATGGAGA GAATACTGCC CAGTGAGAGAA GCCAGGAGAA CGAGGAGGAC GGTGAGGAGG	540

ACCCTGACCG	CTATGTCTGT	AGTGGGGTTC	CCGGGCGGCC	GCCAGGCCTG	GAGGAAGAGC	600
TGACCCCTCAA	ATACGGAGCG	AAGCATGTGA	TCATGTCTGT	TGTGCCTGTC	ACTCTGTGCA	660
TGATCGTGGT	GGTAGCCACC	ATCAAGTCTG	TGCGCTTCTA	CACAGAGAAG	AATGGACAGC	720
TCATCTACAC	GCCATTCACT	GAGGACACAC	CCTCGGTGGG	CCAGCGCCTC	CTCAACTCCG	780
TGCTGAACAC	CCTCATCATG	ATCAGCGTCA	TCGTGGTTAT	GACCATCTTC	TTGGTGGTGC	840
TCTACAAGTA	CCGCTGCTAC	AAGTTCATCC	ATGGCTGGTT	GATCATGTCT	TCACTGATGC	900
TGCTGTTCCCT	CTTCACCTAT	ATCTACCTTG	GGGAAGTGCT	CAAGACCTAC	AATGTGGCCA	960
TGGACTACCC	CACCCTCTTG	CTGACTGTCT	GGAACCTTCGG	GGCAGTGGGC	ATGGTGTGCA	1020
TCCACTGGAA	GGGCCCTCTG	GTGCTGCAGC	AGGCCTACCT	CATCATGATC	AGTGCGCTCA	1080
TGGCCCTAGT	GTTTCATCAAG	TACCTCCCAG	AGTGGTCCGC	GTGGGTCATC	CTGGGCGCCA	1140
TCTCTGTGTA	TGATCTCGTG	GCTGTGCTGT	GTCCCAAAGG	GCCTCTGAGA	ATGCTGGTAG	1200
AAACTGCCCA	GGAGAGAAAT	GAGCCCATAT	TCCCTGCCCT	GATATACTCA	TCTGCCATGG	1260
TGTGGACGGT	TGGCATGGCG	AAGCTGGACC	CCTCCTCTCA	GGGTGCCCTC	CAGCTCCCCT	1320
ACGACCCGGA	GATGGAAGAA	GA CTCCTATG	ACAGTTTGG	GGAGCCTTCA	TACCCCGAAG	1380
TCTTTGAGCC	TCCCTTGACT	GGCTACCCAG	GGGAGGAGCT	GGAGGAAGAG	GAGGAAAGGG	1440
GCGTGAAGCT	TGGCCTCGGG	GA CTCATCT	TCTACAGTGT	GCTGGTGGGC	AAGGCGGCTG	1500
CCACGGGCAG	CGGGGACTGG	AATACCACGC	TGGCCTGCTT	CGTGGCCATC	CTCATTGGCT	1560
TGTGTCTGAC	CCTCCTGCTG	CTTGCTGTGT	TCAAGAAGGC	GCTGCCCGCC	CTCCCCATCT	1620
CCATCACGTT	CGGGCTCATC	TTTTACTTCT	CCACGGACAA	CCTGGTGCGG	CCGTTCATGG	1680
ACACCCTGGC	CTCCCATCAG	CTCTACATCT	GAGGGACATG	GTGTGCCACA	GGCTGCAAGC	1740
TGCAGGGAAT	TTTCATTGGA	TGCAGTTGTA	TAGTTTTACA	CTCTAGTGCC	ATATATTTTT	1800
AAGACTTTTC	TTTCCTTAAA	AAATAAAGTA	CGTGTTTACT	TGGTGAGGAG	GAGGCAGAAC	1860
CAGCTCTTTG	GTGCCAGCTG	TTTCATCACC	AGACTTTGGC	TCCCGCTTTG	GGGAGCGCCT	1920
CGCTTCACGG	ACAGGAAGCA	CAGCAGGTTT	ATCCAGATGA	ACTGAGAAGG	TCAGATTAGG	1980
GTGGGGAGAA	GAGCATCCGG	CATGAGGGCT	GAGATGCCCA	AAGAGTGTGC	TCGGGAGTGG	2040
CCCCTGGCAC	CTGGGTGCTC	TGGCTGGAGA	GGAAAAGCCA	GTTCCCTACG	AGGAGTGTTT	2100
CCAATGCTTT	GTCCATGATG	TCCTTGTTAT	TTTATTNCCY	TTANAACTG	ANTCCTNTTN	2160
TTNTTDCGGC	AGTCACMCTN	CTGGGRAGTG	GCTTAATAGT	AANATCAATA	AANAGNTGAG	2220
TCCTNTTAGA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2280
AAAAA						2285

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Met	Leu	Thr	Phe	Met	Ala	Ser	Asp	Ser	Glu	Glu	Glu	Val	Cys	Asp	Glu	1	5	10	15
Arg	Thr	Ser	Leu	Met	Ser	Ala	Glu	Ser	Pro	Thr	Pro	Arg	Ser	Cys	Gln	20	25	30	
Glu	Gly	Arg	Gln	Gly	Pro	Glu	Asp	Gly	Glu	Asn	Thr	Ala	Gln	Trp	Arg	35	40	45	
Ser	Gln	Glu	Asn	Glu	Glu	Asp	Gly	Glu	Glu	Asp	Pro	Asp	Arg	Tyr	Val	50	55	60	
Cys	Ser	Gly	Val	Pro	Gly	Arg	Pro	Pro	Gly	Leu	Glu	Glu	Glu	Leu	Thr	65	70	75	80
Leu	Lys	Tyr	Gly	Ala	Lys	His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	85	90	95	
Leu	Cys	Met	Ile	Val	Val	Val	Ala	Thr	Ile	Lys	Ser	Val	Arg	Phe	Tyr	100	105	110	
Thr	Glu	Lys	Asn	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	115	120	125	
Pro	Ser	Val	Gly	Gln	Arg	Leu	Leu	Asn	Ser	Val	Leu	Asn	Thr	Leu	Ile	130	135	140	
Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu	Val	Val	Leu	Tyr	145	150	155	160
Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu	Ile	Met	Ser	Ser	165	170	175	
Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu	Gly	Glu	Val	Leu	180	185	190	
Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu	Leu	Leu	Thr	Val	195	200	205	
Trp	Asn	Phe	Gly	Ala	Val	Gly	Met	Val	Cys	Ile	His	Trp	Lys	Gly	Pro	210	215	220	
Leu	Val	Leu	Gln	Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	225	230	235	240
Leu	Val	Phe	Ile	Lys	Tyr	Leu	Pro	Glu	Trp	Ser	Ala	Trp	Val	Ile	Leu	245	250	255	
Gly	Ala	Ile	Ser	Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	260	265	270	
Pro	Leu	Arg	Met	Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Pro	Ile	275	280	285	
Phe	Pro	Ala	Leu	Ile	Tyr	Ser	Ser	Ala	Met	Val	Trp	Thr	Val	Gly	Met	290	295	300	

Ala	Lys	Leu	Asp	Pro	Ser	Ser	Gln	Gly	Ala	Leu	Gln	Leu	Pro	Tyr	Asp	
305					310					315					320	
Pro	Glu	Met	Glu	Glu	Asp	Ser	Tyr	Asp	Ser	Phe	Gly	Glu	Pro	Ser	Tyr	
				325					330					335		
Pro	Glu	Val	Phe	Glu	Pro	Pro	Leu	Thr	Gly	Tyr	Pro	Gly	Glu	Glu	Leu	
			340					345					350			
Glu	Glu	Glu	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	Asp	Phe	Ile	
		355					360					365				
Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ala	Ala	Thr	Gly	Ser	Gly	Asp	
	370					375					380					
Trp	Asn	Thr	Thr	Leu	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	Gly	Leu	Cys	
385					390					395					400	
Leu	Thr	Leu	Leu	Leu	Leu	Ala	Val	Phe	Lys	Lys	Ala	Leu	Pro	Ala	Leu	
				405					410					415		
Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Ile	Phe	Tyr	Phe	Ser	Thr	Asp	Asn	
			420				425						430			
Leu	Val	Arg	Pro	Phe	Met	Asp	Thr	Leu	Ala	Ser	His	Gln	Leu	Tyr	Ile	
		435					440					445				

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	His	Val	Ile	Met	Leu	Phe	
1				5					10					15		
Val	Pro	Val	Thr	Leu	Cys	Met	Ile	Val	Val	Val	Ala	Thr	Ile	Lys	Ser	
			20				25						30			
Val	Arg	Phe	Tyr	Thr	Glu	Lys	Asn	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	
	35					40						45				
Thr	Glu	Asp	Thr	Pro	Ser	Val	Gly	Gln	Arg	Leu	Leu	Asn	Ser	Val	Leu	
	50				55						60					
Asn	Thr	Leu	Ile	Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu	
65				70					75						80	
Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu	
			85					90						95		
Ile	Met	Ser	Ser	Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu	
		100						105					110			
Gly	Glu	Val	Leu	Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu	
		115					120					125				

Leu	Leu	Thr	Val	Trp	Asn	Phe	Gly	Ala	Val	Gly	Met	Val	Cys	Ile	His
130						135					140				
Trp	Lys	Gly	Pro	Leu	Val	Leu	Gln	Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser
145					150					155					160
Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr	Leu	Pro	Glu	Trp	Ser	Ala
				165					170					175	
Trp	Val	Ile	Leu	Gly	Ala	Ile	Ser	Val	Tyr	Asp	Leu	Val	Ala	Val	Leu
			180					185					190		
Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg
		195					200					205			
Asn	Glu	Pro	Ile	Phe	Pro	Ala	Leu	Ile	Tyr	Ser	Ser	Ala	Met	Val	Trp
	210					215					220				
Thr	Val	Gly	Met	Ala	Lys	Leu	Asp	Pro	Ser	Ser	Gln	Gly	Ala	Leu	Gln
225					230					235					240
Leu	Pro	Tyr	Asp	Pro	Glu	Met	Glu	Glu	Asp	Ser	Tyr	Asp	Ser	Phe	Gly
				245					250					255	
Glu	Pro	Ser	Tyr	Pro	Glu	Val	Phe	Glu	Pro	Pro	Leu	Thr	Gly	Tyr	Pro
			260					265					270		
Gly	Glu	Glu	Leu	Glu	Glu	Glu	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu
		275					280					285			
Gly	Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ala	Ala	Thr
	290					295					300				
Gly	Ser	Gly	Asp	Trp	Asn	Thr	Thr	Leu	Ala	Cys	Phe	Val	Ala	Ile	Leu
305					310					315					320
Ile	Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Val	Phe	Lys	Lys	Ala
				325					330					335	
Leu	Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Ile	Phe	Tyr	Phe
			340					345					350		
Ser	Thr	Asp	Asn	Leu	Val	Arg	Pro	Phe	Met	Asp	Thr	Leu	Ala	Ser	His
		355					360					365			
Gln	Leu	Tyr	Ile												
			370												

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGTACCGCCA CCATGACAGA GGTACCTGCA C 31

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCACTG GCTGTAGAAA AAGAC 25

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCGGTC CACTTCGTAT GCTG 24

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTTTTTGAAT TCTTAGGCTA TGGTTGTGTT CCA 33

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid



(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATTAGTGGT TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATTAGTGGC TGTTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTTTTCCAGC TCTCATTTA

19

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TTTTTCCAGT TCTCATTTA

19

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:  
 TACAGTGTTC TGGTTGGTA 19

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:  
 TACAGTGTTC TGGTTGGTA 19

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:  
 TACAGTGTTC TGGTTGGTA 19

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1092 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCTAGATAA GNCAACATTC AGGGGTAGAA GGGGACTGTT TATTTTTTCC TTTAGTCTCT	60
CTTAAAGAGT GAGAAAAATT TTCCCAGGAA TCCCAGGTGGA CTTTGCTTCA CCACTCATAG	120
GTTCATACCA AGTTACAACC CCACAACCTT AGAGCTTTTG TTAGGAAGAG GCTTGGTGGG	180
ATTACCGTGC TTGGCTTGGC TTGGTCAGGA TTCACCACCA GAGTCATGTG GGAGGGGGTG	240
GGAACCCAAA CAATTCAGGA TTCTGCCCTC AGGAAATAAA GGAGAAAATA GCTGTTGGAT	300
AAACTACCAG CAGGCACTGC TACAGCCCAT GCTTTGTGGT TTAAGGGCCA GCTAGTTACA	360
ATGACAGCTA GTTACTGTTT CCATGTAATT TTCTTAAAGG TATTAAATTT TTCTAAATAT	420
TAGAGCTGTA ACTTCCACTT TCTCTTGAAG GCACAGWAAG GGAGTCACAA GACACTGTTG	480
CAGAGAATGA TGATGGCGGG TTCAGTGAGG AATGGGAASC CCAGRGGGAC ANTCATCTAG	540
GGCCTCATCG CTCTACACCT GAGTCACGAG CTKCTNTCCA GGRAC'TTCC ANCAGTATCC	600
TCGCTGGTGA AGACCCAGAG GAAAGNATGT TCANTTCTCC ATN'TTTCAA GTCATGGATT	660
CCTTTAGGTA GCTACATTAT CAACCTTTTT GAGAATAAAA TGAATTGAGA GTGTTACAGT	720
CTAATTCTAT ATCACATGTA ACTTTTATTT GGATATATCA GTAATAGTGC TTTT'TYNTT	780
TTTTTTTTTT TTTTTTTTTT TTTTNGGNGA NAGAGTCTCG CTCTGTCGCC AGGTTGGAGT	840
GCAATGGTGC GATCTTGGCT CACTGAAAGC TCCACCNCCC GGGTTCAAGT GATTCTCCTG	900
CCTCAGCCNC CCAAGTAGNT GGGACTACAG GGGTGCGCCA CCACGCCTGG GATAATTTTG	960
GGNTTTTTTAG TAGAGATGGC GTTTCACCAN CTTGGNGCAG GCTGGTCTTG GAACTCCTGA	1020
NATCATGATC TGCCTGCCTT AGCCTCCCCA AAGTGCTGGG ATTNCAGGGG TGAGCCACTG	1080
TTCCTGGGCC TC	1092

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1003 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGCAGTGAG CCGAGATCAT GCTGCTGTAC TCCAGCCTGG GCCACAGAGC CAAACTCCAT	60
CTCCCAAAAA AAAAAAATAT TAATTAATAT GATNAAATGA TGCCTATCTC AGAATTCTTG	120
TAAGGATTTC TTAGKACAAG TGCTGGGTAT AAACTATANA TTCRATAGAT GNCGATTATT	180
ACTTAYTATT GTTATTGATA AATAACAGCA GCATCTACAG TTAAGACTCC AGAGTCAGTC	240
ACATAGAATC TGGNACTCCT ATTGTAGNAA ACCCCNMAG AAAGAAAACA CAGCTGAAGC	300
CTAATTTTGT ATATCATTTA CTGACTTCTC TCATTCAATTG TGGGGTTGAG TAGGGCAGTG	360
ATATTTTGA ATTGTGAAAT CATANCAAAG AGTGACCAAC TTTTAAATAT TTGTAACCTT	420

TCCTTTTATAG	GGGGAGTAAA	ACTTGGATTG	GGAGATTTC	TTTTCTACAG	TGTTCTGGTT	480
GGTAAAGCCT	CAGCAACAGC	CAGTGGAGAC	TGGAACACAA	CCATAGCCTG	TTTCGTAGCC	540
ATATTAATTG	TMMSTATACA	CTAATAAGAA	TGTGTCAGAG	CTCTTAATGT	CMAAACTTTG	600
ATTACACAGT	CCCTTTAAGG	CAGTTCTGTT	TTAACCCCAG	GTGGGTAAA	TATTCCAGCT	660
ATCTGAGGAG	CTTTTNGATA	ATTGGACCTC	ACCTTAGTAG	TTCTCTACCC	TGGCCACACA	720
TTAGAATCAC	TTGGGAGCTT	TTAAACTGT	AAGCTCTGCC	CTGAGATATT	CTTACTCAAT	780
TTAATTGTGT	AGTTTTTAAA	ATTCCCCAGG	AAATTCTGGT	ATTTCTGTTT	AGGAACCGCT	840
GCCTCAAGCC	TAGCAGCACA	GATATGTAGG	AAATTAGCTC	TGTAAGGTTG	GTCTTACAGG	900
GATAAACAGA	TCCTTCCTTA	GTCCTGGAC	TTAATCACTG	AGAGTTTGGG	TGGTGGTTTT	960
GGATTTAATG	ACACAACCTG	TAGCATGCAG	TGTTACTTAA	GAC		1003

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1726 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGATCCCTCC	CCTTTTTAGA	CCATACAAGG	TAACTTCCGG	ACGTTGCCAT	GGCATCTGTA	60
AACTGTCATG	GTGTTGGCGG	GGAGTGTCTT	TTAGCATGCT	AATGTATTAT	AATTAGCGTA	120
TAGTGAGCAG	TGAGGATAAC	CAGAGGTCAC	TCTCCTCACC	ATCTTGTTTT	TGGTGGGTTT	180
TGGCCAGCTT	CTTTATTGCA	ACCAGTTTTA	TCAGCAAGAT	CTTTATGAGC	TGTATCTTGT	240
GCTGACTTCC	TATCTCATCC	CGNAACTAAG	AGTACCTAAC	CTCCTGCAAA	TTGMAGNCCA	300
GNAGGTCTTG	GNCTTATTTN	ACCCAGCCCC	TATTCAARAT	AGAGTNGYTC	TTGGNCCAAA	360
CGCCYCTGAC	ACAAGGATTT	TAAAGTCTTA	TTAATTAAGG	TAAGATAGKT	CCTTGSATAT	420
GTGGTCTGAA	ATCACAGAAA	GCTGAATTTG	GAAAAAGGTG	CTTGGASCTG	CAGCCAGTAA	480
ACAAGTTTTC	ATGCAGGTGT	CAGTATTTAA	GGTACATCTC	AAAGGATAAG	TACAATTGTG	540
TATGTTGGGA	TGAACAGAGA	GAATGGAGCA	ANCCAAGACC	CAGGTAAAAG	AGAGGACCTG	600
AATGCCTTCA	GTGAACAATG	ATAGATAATC	TAGACTTTTA	AACTGCATAC	TTCCTGTACA	660
TTGTTTTTTC	TTGCTTCAGG	TTTTTAGAAC	TCATAGTGAC	GGGTCTGTTG	TTAATCCCAG	720
GTCTAACCGT	TACCTTGATT	CTGCTGAGAA	TCTGATTTAC	TGAAAATGTT	TTTCTTGTGC	780
TTATAGAATG	ACAATAGAGA	ACGGCAGGAG	CACAACGACA	GACGGAGCCT	TGGCCACCCT	840

GANCCATTAT	CTAATGGACG	ACCCAGGGTA	ACTCCCGGCA	GGTGGTGGAN	CAAGATGAGG	900
AAGAAGATGA	GGANCTGACA	TTGAAATATG	NCGSCAAGCA	TGTGATCATG	CTCTTTGKCC	960
CTGTGACTCT	CTGCATGGTG	GTGGTCGTGG	NTACCATTAA	GTCAGTCAGC	TTTTATACCC	1020
GGAAGGATGG	GCAGCTGTAC	GTATGAGTTT	KGTTTTATTA	TTCTCAAASC	CAGTGTGGCT	1080
TTTCTTTACA	GCATGTCATC	ATCACCTTGA	AGGCCTCTNC	ATTGAAGGGG	CATGACTTAG	1140
CTGGAGAGCC	CATCCTCTGT	GATGGTCAGG	AGCAGTTGAG	AGANCGAGGG	GTTATTACTT	1200
CATGTTTTAA	GTGGAGAAAA	GGAACACTGC	AGAAGTATGT	TTCCTGTATG	GTATTACTGG	1260
ATAGGGCTGA	AGTTATGCTG	AATTGAACAC	ATAAATTCTT	TTCCACCTCA	GGGNCATTGG	1320
GCGCCCATTG	NTCTTCTGCC	TAGAATATTC	TTTCCTTTNC	TNACTTKGGN	GGATTAAATT	1380
CCTGTCATCC	CCCTCCTCTT	GGTGTTATAT	ATAAAGTNTT	GGTGCCGCAA	AAGAAGTAGC	1440
ACTCGAATAT	AAAATTTTCC	TTTTAATTCT	CAGCAAGGNA	AGTTACTTCT	ATATAGAAGG	1500
GTGCACCCNT	ACAGATGGAA	CAATGGCAAG	CGCACATTTG	GGACAAGGGA	GGGGAAAGGG	1560
TTCTTATCCC	TGACACACGT	GGTCCCNGCT	GNTGTGTNCT	NCCCCACTG	ANTAGGGTTA	1620
GACTGGACAG	GCTTAAACTA	ATTCCAATTG	GNTAATTTAA	AGAGAATNAT	GGGGTGAATG	1680
CTTTGGGAGG	AGTCAAGGAA	GAGNAGGTAG	NAGGTAACCT	GAATGA		1726

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNCGTATAAA	AGACCAACAT	TGCCANCNAC	AACCACAGGC	AAGATCTTCT	CCTACCTTCC	60
CCCNNGGTGT	AATACCAAGT	ATTCNCCAAT	TTGTGATAAA	CTTTCATTGG	AAAGTGACCA	120
CCCTCCTTGG	TTAATACATT	GTCTGTGCCT	GCTTTCACAC	TACAGTAGCA	CAGTTGAGTG	180
TTTGCCCTGG	AGACCATATG	ACCCATAGAG	CTTAAAATAT	TCAGTCTGGC	TTTTTACAGA	240
GATGTTTCTG	ACTTTGTAA	TAGAAAATCA	ACCCAAGTGG	TTTAAATAAT	GCACATACTT	300
TCTCTCTCAT	AGAGTAGTGC	AGAGGTAGNC	AGTCCAGATT	AGTASGGTGG	CTTCACGTTC	360
ATCCAAGGAC	TCAATCTCCT	TCTTTCTTCT	TTAGCTTCTA	ACCTCTAGCT	TACTTCAGGG	420
TCCAGGCTGG	AGCCCTASCC	TTCATTTCTG	ACAGTAGGAA	GGAGTAGGGG	AGAAAAGAAC	480
ATAGGACATG	TCAGCAGAAT	TCTCTCCTTA	GAAGTTCCAT	ACACAACACA	TCTCCCTAGA	540
AGTCATTGCC	CTTACTTGTT	CTCATAGCCA	TCCTAAATAT	AAGGGAGTCA	GAAGTAAAGT	600

CTKKNTGGCT	GGGAATATTG	GCACCTGGAA	TAAAAATGTT	TTTCTGTGAA	TGAGAAACAA	660
GGGGAAGATG	GATATGTGAC	ATTATCTTAA	GACAACTCCA	GTTGCAATTA	CTCTGCAGAT	720
GAGAGGCACT	AATTATAAGC	CATATTACCT	TTCTTCTGAC	AACCACTTGT	CAGCCCNCGT	780
GGTTTCTGTG	GCAGAATCTG	GTTCYATAMC	AAGTTCCTAA	TAANCTGTAS	CCNAAAAAAT	840
TTGATGAGGT	ATTATAATTA	TTTCAATATA	AAGCACCCAC	TAGATGGAGC	CAGTGTCTGC	900
TTCACATGTT	AAGTCCTTCT	TTCCATATGT	TAGACATTTT	CTTTGAAGCA	ATTTTAGAGT	960
GTAGCTGTTT	TTCTCAGGTT	AAAAATTCTT	AGCTAGGATT	GGTGAGTTGG	GGAAAAGTGA	1020
CTTATAAGAT	NCGAATTGAA	TTAAGAAAAA	GAAAATTCTG	TGTTGGAGGT	GGTAATGTGG	1080
KTGGTGATCT	YCATTAAACAC	TGANCTAGGG	CTTTKGKGTT	TGKTTTATTG	TAGAATCTAT	1140
ACCCCATTC	NAGAAGATAC	CGAGACTGTG	GGCCAGAGAG	CCCTGCACTC	AATTCTGAAT	1200
GCTGCCATCA	TGATCAGNGT	CATTGTWGTC	ATGACTANNC	TCCTGGTGGT	TCWGTATAAA	1260
TACAGGTGCT	ATAAGGTGAG	CATGAGACAC	AGATCTTTGN	TTTCCACCCT	GTTCTTCTTA	1320
TGGTTGGGTA	TTCTTGTGAC	AGTAACTTAA	CTGATCTAGG	AAAGAAAAAA	TGTTTTGTCT	1380
TCTAGAGATA	AGTTAATTTT	TAGTTTTCTT	CCTCCTCACT	GTGGAACATT	CAAAAAATAC	1440
AAAAAGGAAG	CCAGGTGCAT	GTGTAATGCC	AGGCTCAGAG	GCTGAGGCAG	GAGGATCGCT	1500
TGGGCCCAGG	AGTTCACAAG	CAGCTTGGGC	AACGTAGCAA	GACCCTGCCT	CTATTAAAGA	1560
AAACAAAAAA	CAAATATTGG	AAGTATTTTA	TATGCATGGA	ATCTATATGT	CATGAAAAAA	1620
TTAGTGTA	ATATATATAT	TATGATTAGN	TATCAAGATT	TAGTGATAAT	TTATGTTATT	1680
TTGGGATTT	AATGCCTTTT	TAGGCCATTG	TCTCAAMAAA	TAAAAGCAGA	AAACAAAAAA	1740
AGTTGTAACT	GAAAAATAAA	CATTTCCATA	TAATAGCACA	ATCTAAGTGG	GTTTTTGNTT	1800
GTTTGTGTT	TTGTTGAAGC	AGGGCCTTGC	CCTNYCACCC	AGGNTGGAGT	GAAGTGCAGT	1860
GGCACGATTT	TGGCTCACTG	CAG				1883

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGTTTGACA	ATTTCTCCGT	TCCACCCTTG	ATTAAATAAG	GTAGTATTCA	TTTTTTAAGT	60
TTTAGCTTTT	GGATATATGT	GTAAGTGTGG	TATGCTGTCT	AATGAATTAA	GACAAATTGGT	120

NCTKTCTTTA	CCCMACANCT	GGACMAAGAG	CAGGCAAGAT	NCAANAATCA	AGTGACCCAG	180
NCAAACCAGA	CACATTTTCT	GCTCTCAGCT	AGCTTGCCAC	CTAGAAAGAC	TGGTTGTCNA	240
AGTTGGAGTC	CAAGAATCGC	GGAGGATGTT	TAAAATGCAG	TTTCTCAGGT	TCTCNCCACC	300
CACCAGAAGT	TTTGATTTCAT	TGAGTGGTGG	GAGAGGGCAG	AGATATTTGC	GATTTTAAACA	360
GCATTCTCTT	GATTGTGATG	CAGCTGGTTC	SCAAATAGGT	ACCCTAAAGA	AATGACAGGT	420
GTAAATTTA	GGATGGCCAT	CGCTTGATG	CCGGGAGAAG	CACACGCTGG	GCCCAATTTA	480
TATAGGGGCT	TTCGTCCTCA	GCTCGAGCAR	CCTCAGAACC	CCGACAACCY	ACGCCAGCKC	540
TCTGGGCGGA	TTCCRTCAGK	TGGGGAAGSC	CAGGTGGAGC	TCTGGKTTCT	CCCCGCAATC	600
GTTTCTCCAG	GCCGGAGGCC	CCGCCCCCTT	CCTCCTGGCT	CCTCCCCCTC	TCCGTGGGCC	660
GNCCGCCAAC	GACGCCAGAG	CCGGAAATGA	CGACAACGGT	GAGGGTTCTC	GGGCGGGGCC	720
TGGGACAGGC	AGCTCCGGGG	TCCNCGNWT	NACATCGGAA	ACAAAACAGC	GGCTGGTCTG	780
GAAGGAACCT	GAKTACGAC	CCGCGGCGGC	AGCGGGGCGG	CGGGGAAGCG	TATGTGCGTG	840
ATGGGGAGTC	CGGGCAAGCC	AGGAAGGCAC	CGCGGACATG	GGCGGCCGCG	GGCAGGGNCC	900
GGNCCTTTGT	GGCCGCCCGG	GCCGCGAAGC	CGGTGTCCTA	AAAGATGAGG	GGCGGGGCGC	960
GGCCGGTTGG	GGCTGGGGAA	CCCCGTGTGG	GAAACCAGGA	GGGGCGGCC	GTTTCTCGGG	1020
CTTCGGGCGC	GGCCGGGTGG	AGAGAGATTC	CGGGGAGCCT	TGGTCCGGA	ATGCTGTTTG	1080
CTCGAAGACG	TCTCAGGGCG	CAGGTGCCTT	GGGCCGGGAT	TAGTAGCCGT	CTGAACTGGA	1140
GTGGAGTAGG	AGAAAGAGGA	AGCGTCTTGG	GCTGGGTCTG	CTTGAGCAAC	TGGTGAAACT	1200
CCGCGCCTCA	CGCCCCGGGT	GTGTCCTTGT	CCAGGGGCGA	CGAGCATTCT	GGGCGAAGTC	1260
CGCACGCCTC	TTGTTTCGAGG	CGGAAGACGG	GGTCTTGATG	CTTTCTCCTT	GGTCGGGACT	1320
GTCTCGAGGC	ATGCATGTCC	AGTGACTCTT	GTGTTTGCTG	CTGCTTCCCT	CTCAGATTCT	1380
TCTCACCGTT	GTGGTCAGCT	CTGCTTTAGG	CATATTAATC	CATAGTGGAG	GCTGGGATGG	1440
GTGAGAGAAT	TGAGGTGACT	TTTCCATAAT	TCAGGTGAGA	TGTGATTAGA	GTYCGGATCC	1500
TNCGGTGGTG	GCAGAGGCTT	ACCAAGAAAC	ACTAACGGGA	CATGGGAACC	AATTGAGGAT	1560
CCAGGGAATA	AAGTGTGAAG	TTGACTAGGA	GGTTTTTCAGT	TTAAGAACAT	GGCAGAGACA	1620
TTCTCAGAAA	TAAGGAAGTT	AGGAAGAAAG	ACCTGGTTTA	GAGAGGAGGG	CGAGGAAGTG	1680
GTTTGGAAGT	GTCACTTTGG	AAGTGCCAGC	AGGTGAAAAT	GCCCTGTGAA	CAGGACTGGA	1740
GCTGAAAACA	GGAATCAATT	CCATAGATTT	CCAGTTGATG	TTGGAGCAGT	GGAGAAAGTCT	1800
AANCTAAGGA	AGGGGAAGAG	GAGGCCAAGC	CAAACACTTA	GGAACACTTN	CNACGAGGGG	1860
GTGGAAGAAG	AGCAAGGAGC	CAGCTGAGGA	GAATGAGTGT	GGTTGGAGAA	CCACCACAGC	1920
NCAGGGTCGC	CAGANCTGAG	GAAGGGGAGG	GAAGCTTATC	GAGKAMSGWC	RACMKCGAGT	1980
TGGCAGGGAT						1990

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 736 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTCCCA TCTTCTCCAC AGAGTTTGTG CCTTACATTA TTACTCCTTG CCATTTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTTGGG CTTGTTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTTT ATATCTAGCA	180
TATTTGCGGT TAGAATCCCA TGGATGTTTC TTCTTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCC GGCTGG ACTTTTGGAG	300
GTTCTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA	360
GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA	420
GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCATCAGC	480
AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGA CTACCGT	540
TACCAAGAGG TTAGGTGAAG TGGTTTAAAC CAAACGGAAC TCTTCATCTT AACTACACG	600
TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTTCAG GAGGTACTGT	660
GAGGAAGAGC AGGCACCACC AGCAGAATGG GGAATGGAGA GGTGGGCAGG GGTTCAGCT	720
TCCCTTTGAT TTTTGT	736

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1117 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNNWGTA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240



AAATGATTTT	ATGAAAATAT	AAAGATTAGN	TTGAGTTTGG	GCCAGCATAG	AAAAAGGAAT	300
GTTGAGAACA	TTCCNTTAAG	GATTACTCAA	GCYCCCCTTT	TGSTGKNWAA	TCAGANNGTC	360
ATNNAMNTAT	CNTNTGTGGG	YTGAAAATGT	TTGGTTGTCT	CAGGCGGTTC	CTACTTATTG	420
CTAAAGAGTC	CTACCTTGAG	CTTATAGTAA	ATTTGTCAGT	TAGTTGAAAG	TCGTGACAAA	480
TTAATACATT	CCTGGTTTAC	AAATTGGTCT	TATAAGTATT	TGATTGGTNT	AAATGNATTT	540
ACTAGGATTT	AACTAACAAT	GGATGACCTG	GTGAAATCCT	ATTTGAGACC	TAATCTGGGA	600
GCCTGCAAGT	GACAACAGCC	TTTGCGGTCC	TTAGACAGCT	TGGCCTGGAG	GAGAACACAT	660
GAAAGAMMGG	TTTGWNTCTG	NTTAWTGTA	TCTATGRAAG	TGTTTTTWAT	MACAGTATAA	720
TTGTMGTMAC	AAAGTTCTGT	TTTTCTTTCC	CTTNCAGAA	CCTCAAGAGG	CTTTGTTTTT	780
TGTGAAACAG	TATTTCTATA	CAGNTGCTCC	AATGACAGAG	TNACCTGCAC	CGTTGTCCTA	840
CTTCCAGAAT	GCACAGATGT	CTGAGGACAA	CCACCTGAGC	AATACTGTAC	GTAGCCAGGT	900
ACAGCGTCAG	TYTCTNAAAC	TGCCTYYGNC	AGACTGGATT	CACTTATCAT	CTCCCCTCAC	960
CTCTGAGAAA	TGCTGAGGGG	GSTAGGNAGG	GCTTTCTCTA	CTTNACCACA	TTTNATAATT	1020
ATTTTTGGGT	GACCTTCAGC	TGATCGCTGG	GAGGGACACA	GGGCTTNTTT	AACACATAGG	1080
GTGTTGGATA	CAGNCCCTCC	CTAATTCACA	TTTCANC			1117

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGCAGCTTT	CCTTTAAACT	AGGAAGACTT	GTTCTATAC	CCCAGTAACG	ATACACTGTA	60
CACTAAGCAA	ATAGCAGTCA	AACCCAAATG	AAATTTNTAC	AGATGTTCTG	TGTCATTTTA	120
TNTTGTTTAT	GTTGTCTCCC	CCACCCCCAC	CAGTTCACCT	GCCATTTATT	TCATATTCAT	180
TCAACGTCTN	NNTGTGTA	AAGAGACAAA	AAACATTAAA	CTTTTTTCCT	TCGTTAATTC	240
CTCCCTACCA	CCCATTTACA	AGTTTAGCCC	ATACATTTTA	TTAGATGTCT	TTTATGTTTT	300
TCTTTTNCTA	GATTTAGTGG	CTGTTTNGTG	TCCGAAAGGT	CCACTTCGTA	TGCTGGTTGA	360
AACAGCTCAG	GAGAGAAATG	AAACGCTTTT	TCCAGCTCTC	ATTTACTCCT	GTAAGTATTT	420
GGAGAATGAT	ATTGAATTAG	TAATCAGNGT	AGAATTTATC	GGGAACTTGA	AGANATGTNA	480
CTATGGCAAT	TTCANGGNAC	TTGTCTCATC	TTAAATGANA	GNATCCCTGG	ACTCCTGNAG	540

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 509 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCCCGTCNAT GCATACTTTG TGTGTCCAGT GCTTACCTGG AATCCNGTCT TTCCCAACAG	60
CAACAATGGT GTGGTTGGTG AATATGGCAG AAGGAGACCC GGAAGCTCAA AGGAGAGTAT	120
CCAAAAATTC CAAGTATAAT GCAGAAAGTA GGTAACCTYYY NTTAGATAMN ATCTTGATTT	180
TNCAGGGTCA CTGTTATAAG CTAACAGTAT AGNAATGTTT TTATCGTCTT TCTNKGGNCA	240
TAGACTCCTN KGAGAATCTC TTGAGAACTA TGATAATGCC CAGTAAATAC NCAGATAAGT	300
ATTTAAGGAG TNCAGATACT CAAANCCCAA CAATACNGTC AAAGCATCCT AGGTTAAGAC	360
AMCNCCCATT AAATACAGAA TACCAGCATG GAAAGGTTCA GGCTGAGGTT ATGATTGGGT	420
TTGGGTTTTG GGNNGTTTTT TTATAAGTCA TGATTTTAAA AAGAAAAAAT AAACCTCTCTC	480
CAAACATGTA AAAGTAAGAA TCTCCTAAA	509

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 823 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CAGGAGTGGA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCNG GGACATAGTG	60
GTACACANCT GTAATGCTCA NCACTKATGG GGAGTACTGA AGNGGNSGG ATCACTTGNG	120
GGTCNGGAAT NTGAGANCAG CCTGGGCAAN ATGGCGAAAC CCTGTCTCTA CTAAAAATAG	180
CCANAAWNWA GCCTAGCGTG GTGGCGCRCA CGCGTGTTTC CACCTACTCA GGAGGCNTAA	240
GCACGAGNAN TNCTTGAACC CAGGAGGCAG AGGNTGTGGT GARCTGAGAT CGTGCCACTG	300
CACTCCAGTC TGGGCGACMA AGTGAGACCC TGTCTCCNNN AAGAAAAAAA AAATCTGTAC	360
TTTTTAAGGG TTGTGGGACC TGTTAATTAT ATTGAAATGC TTCTYTTCTA GGTCATCCAT	420
GCCTGGCTTA TTATATCATC TCTATTGTTG CTGCTCTTTT TTACATTCAT TTAATTGGGG	480

TAAGTTGTGA AATTTGGGGT CTGTCTTTCA GAATTAACTA CCTNNGTGCT GTGTAGCTAT	540
CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTTAATTGT NTCCACATAT	600
AGGTCATACT TGGTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG	660
CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACTTAAGA CTACAGTTAA TTCTAAGCCT	720
TTGGGGAAGG ATTATATAGC CTTCTAGTAG GAAGTCTTGT GCNATCAGAA TGTTTNTAAA	780
GAAAGGGTNT CAAGGAATNG TATAAANACC AAAAATAATT GAT	823

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTTNTCCNAA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACC AAAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAGA GTAAATTAAT TTANAGGGAA	180
GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240
TTAATATCTA ATGTTTGGGA GCCATCACAT TATTCTAAAT AATGTTTTGG TGGAAATTAT	300
TGTACATCTT TTAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC	480
CCTCATGNCC CTGKTGTTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTTGGC	540
TGTGATTTC A GTATATGGTA AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCCCC	600
ACTGGAGTGT TTTCTTTCCT CATCTCTTTA TCTTGATTGA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAAAT AGCTATAGTA ACTTTTTCAT TTGAAGATTT	720
CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG	780
ATCACCTAAG CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGCACACCTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Tyr Thr Pro Phe  
1

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ser Thr Pro Glu  
1

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTCACTGA GGACACACC

19

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TGTAGAGCAC CACCAAGA

18

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCATGGTGTG CATCCACT

18

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GGACCACTCT GGGAGGTA

18

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AAACTTGGAT TGGGAGAT

18

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn	Asp	Asn	Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Lys	Asp	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Glu	Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	Tyr	Asn	Ala	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ser	His	Leu	Gly	Pro	His	Arg	Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CAGAGGATGG AGAGAATAC

19

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCTCCCCAA AACTGTCAT

19

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCCCTAGTGT TCATCAAGTA

20

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:  
AAAGCGGGAG CCAAAGTC 18

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:  
TCACAGAAGA TACCGAGACT 20

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:  
CCCAACCATA AGAAGAACAG 20

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:  
TCTGTACTTT TTAAGGGTTG TG 22

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ACTTCAGAGT AATTCATCAN CA

22

- (2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GACTCCAGCA GGCATATCT

19

- (2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GATGAGACAA GTNCCNTGAA

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- (2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TTAGTGGCTG TTTNGTGTCC

20

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CACCCATTTA CAAGTTTAGC

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